

FIG. 1A-1

(SEQ ID NO:1)

5' GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT

ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA

(SEQ ID NO:2) → M E S R K D I T N Q E E L W K

ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA

M K P R R N L E E D D Y L H K D T G

GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT

E T S M L K R P V L L H L H Q T A H

GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA

A D E F D C P S E L Q H T Q E L F P

CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT

Q W H L P I K I A A I I A S L T F L

TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT

Y T L L R E V I H P L A T S H Q Q Y

TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC

F Y K I P I L V I N K V L P M V S I

ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT

T L L A L V Y L P G V I A A I V Q L

CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA

H N G T K Y K K F P H W L D K W M L

ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT

T R K Q F G L L S F F F A V L H A I

TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG

Y S L S Y P M R R S Y R Y K L L N W

FIG. 1A-2

659	668	677	686	695	704
GCA TAT CAA CAG GTC	CAA CAA AAT AAA GAA GAT	GCC TGG ATT GAG CAT GAT	GTT		
A Y Q Q V Q Q N K E D A W I E H D V					
713	722	731	740	749	758
TGG AGA ATG GAG ATT TAT GTG TCT CTG GGA ATT GTG GGA TTG GCA ATA CTG GCT					
W R M E I Y V S L G I V G L A I L A					
767	776	785	794	803	812
CTG TTG GCT GTG ACA TCT ATT CCA TCT GTG AGT GAC TCT TTG ACA TGG AGA GAA					
L L A V T S I P S V S D S L T W R E					
821	830	839	848	857	866
TTT CAC TAT ATT CAG AGC AAG CTA GGA ATT GTT TCC CTT CTA CTG GGC ACA ATA					
F H Y I Q S K L G I V S L L L G T I					
875	884	893	902	911	920
CAC GCA TTG ATT TTT GCC TGG AAT AAG TGG ATA GAT ATA AAA CAA TTT GTA TGG					
H A L I F A W N K W I D I K Q F V W					
929	938	947	956	965	974
TAT ACA CCT CCA ACT TTT ATG ATA GCT GTT TTC CTT CCA ATT GTT GTC CTG ATA					
Y T P P T F M I A V F L P I V V L I					
983	992	1001	1010	1019	1028
TTT AAA AGC ATA CTA TTC CTG CCA TGC TTG AGG AAG AAG ATA CTG AAG ATT AGA					
F K S I L F L P C L R K K I L K I R					
1037	1046	1055	1064	1073	1082
CAT GGT TGG GAA GAC GTC ACC AAA ATT AAC AAA ACT GAG ATA TGT TCC CAG TTG					
H G W E D V T K I N K T E I C S Q L					
1091	1100	1109	1118	1127	1136
TAG AAT TAC TGT TTA CAC ACA TTT TTG TTC AAT ATT GAT ATA TTT TAT CAC CAA					
* N Y C L H T F L F N I D I F Y H Q					
1145	1154	1163	1172	1181	1190
CAT TTC AAG TTT GTA TTT GTT AAT AAA ATG ATT ATT CAA GGA AAA AAA AAA AAA					
H F K F V F V N K M I I Q G K K K K					

AAA AA 3'

K

FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3' (SEQ ID NO:3)

FIG. 4A

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC
ATACTATTTTATAGAATTAATGGAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG
AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACCTCTTCCACA
GTGGCACTTGCCAATTAATAAGCTGCTATTATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATT
CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTTCATAATGGAACCAA
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT
ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTATGTGTCTCT
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGAATCTTTGACATGG
AGAGAATTTCACTATATTCAGGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT
ATAGAATATGTTGACTTTACCCCATAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTGTGTTCCAATT
AATAATGTGCTCTCCTGTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTCCTAGACATAAATAAAGGCAT
TAAAATATTCTTTGTTTTTTTTTTTTGTTTGTGTTGTTTTGTTTGTGTTGTTTTGTTTTGAGATGAAGTCTCG
CTCTGTGCCCATGCTGGAGTACAGTGGCAGCATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTC
TCTTGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTAGTA
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC
AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTCTAATATTTGAACTTGTTAGACAATTT
GCTACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTATTATTTCTTAAAAAAATATTCTTTTACC
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACCTAGCACTTTCAGAAACAAAACTCTCTCCTTGAAA
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT
ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGCTGACAAGATTCAAAGGACTAAA
TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTGAGACATT
CGCAACTATCCCTTCTACATGTCCACAGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCTTAATTTGTAGGTTTCAG
CCTGATAACCACTGGAGTTCTTTGGTCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA
TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACA

FIG. 4B

ATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAACTAATTTTCAACCAATGACATGTATTTTCAACT
AGTAACCTAGAAATGTTTCACTTAAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA
ACGCAAACCTAGCTATTTGATTGTATTTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT
GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT
TGAGATTACATAGGTGAACAACTATTTTTAAGCAACTTTATTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA
ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTTCATATTATTTCCATGTTATC
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACCTTCATTATTCAATTTATCAAAATCAGAGTGAATCA
CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTGTCTATAATCTTCAATCTACCTATAT
TTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT
GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAATAAATATCATAAG
GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG
TTCACCTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG
TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG
ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTCTTTTCTTTTGCAGAGCAAGCTAGGA
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTGCCTGGAATAAGTGGATAGATATAAAACAATTG
TATGGTATACACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGTCCTGATATTTAAAGCATACTATT
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACCTGAG
ATATGTTCCCAGTTGTAGAAATTACTGTTTACACACATTTTGTTCATATTGATATATTTTATCACCAACATTTC
AGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:4)

FIG. 5

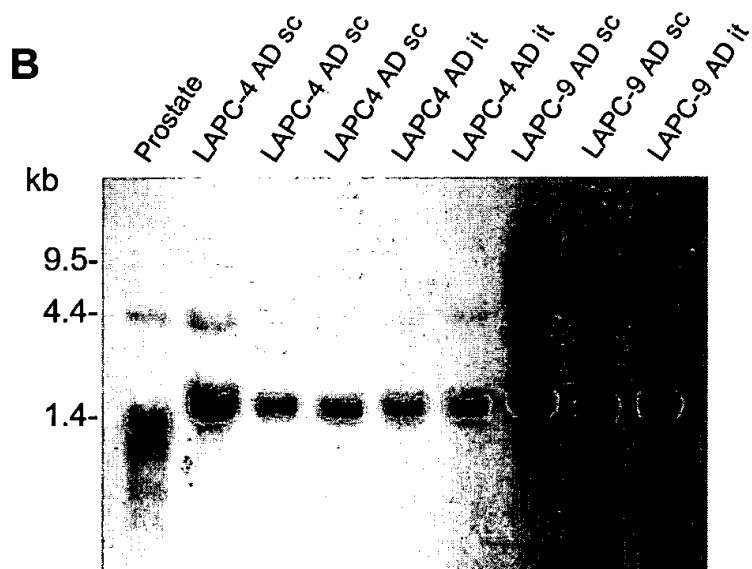
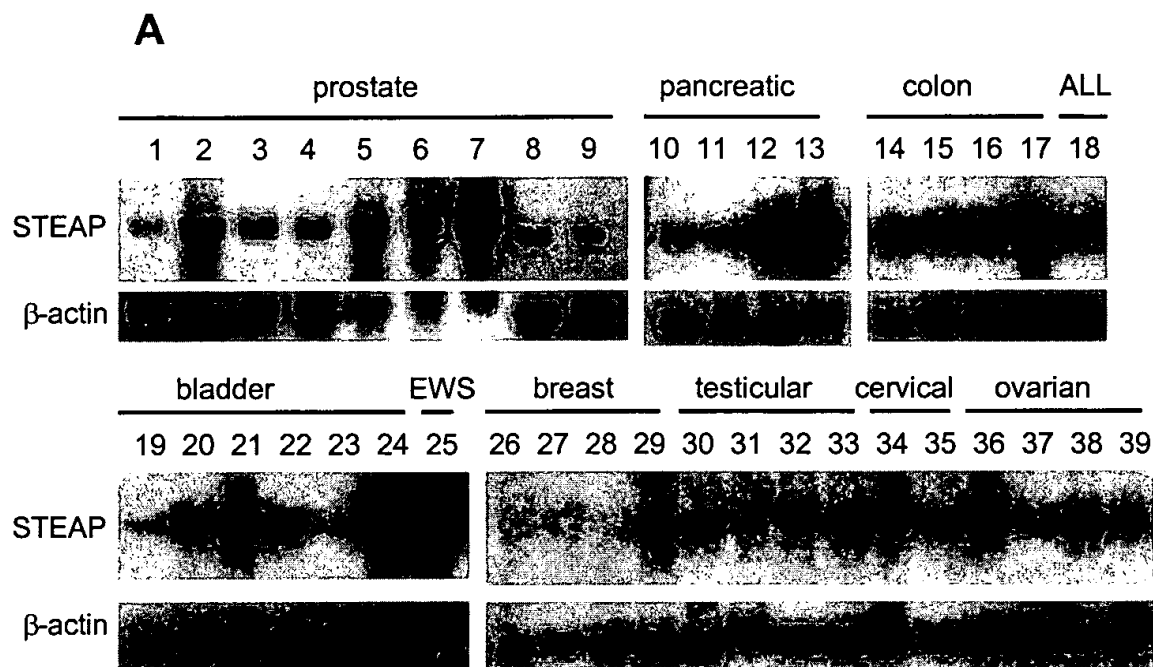


FIG. 6

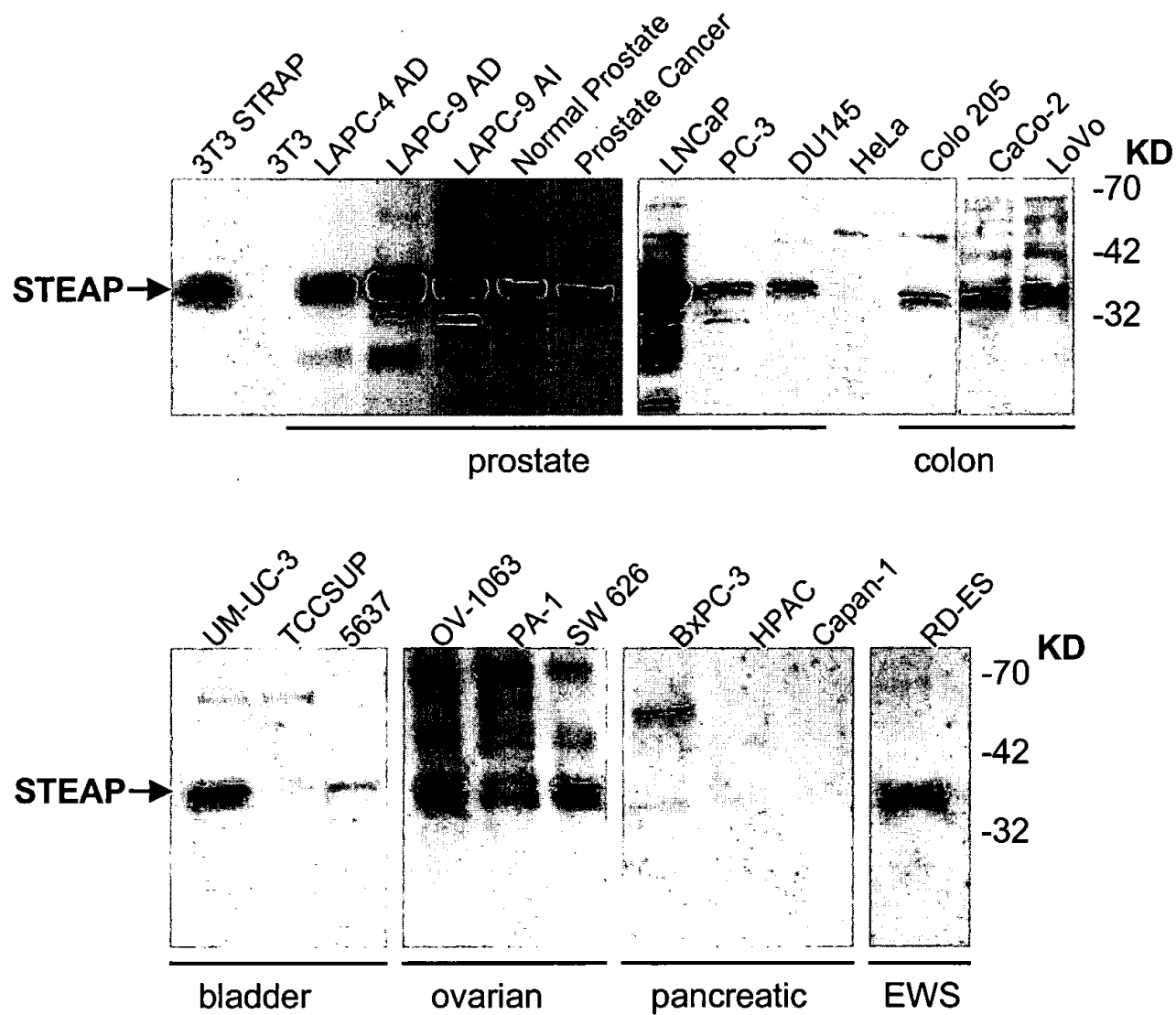
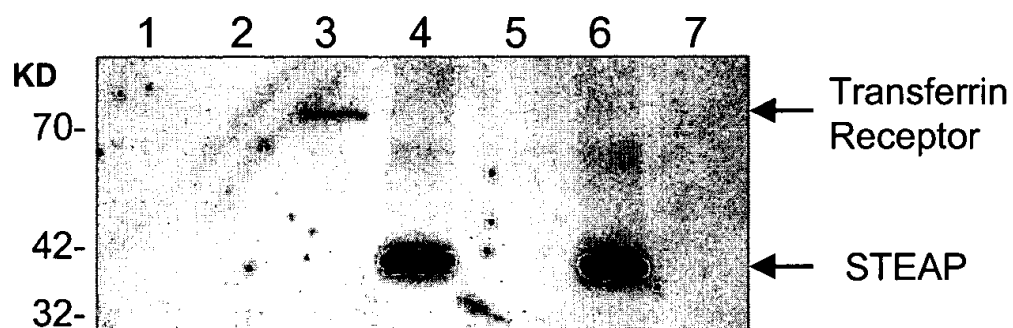


FIG. 7

A



B

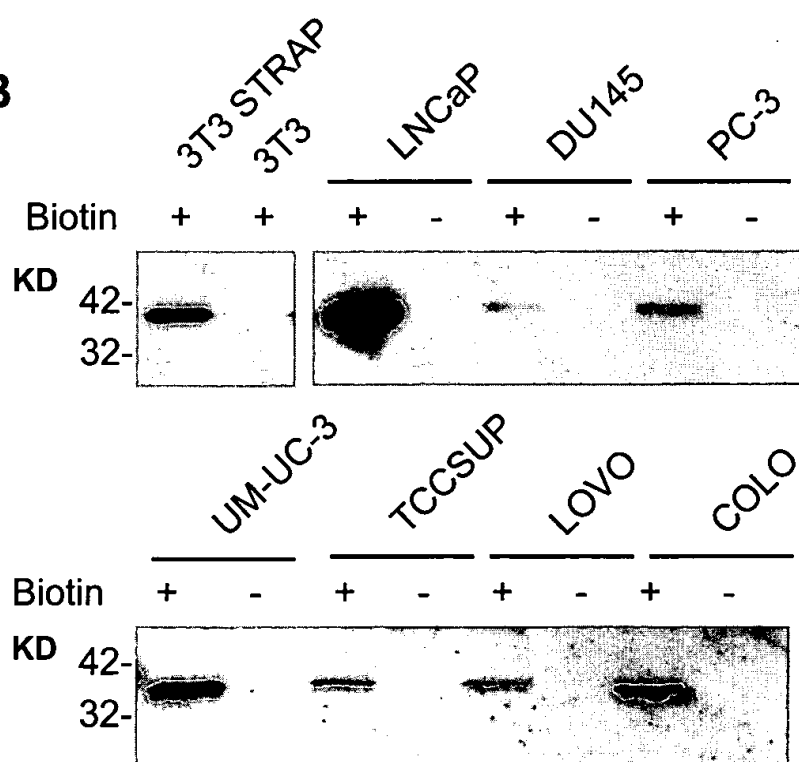


FIG. 9A

(SEQ ID NO:5)

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      10      19      28      37      46      55
5'  GGA CGC GTG GGC GGA CGC GTG GGT TCC TCG GGC CCT CGG CGC CAC AAG CTG TCC
    ---
      64      73      82      91      100      109
    GGG CAC GCA GCC CCT AGC GGC GCG TCG CTG CCA AGC CGG CCT CCG CGC GCC TCC
    ---
      118      127      136      145      154      163
    CTC CTT CCT TCT CCC CTG GCT GTT CGC GAT CCA GCT TGG GTA GGC GGG GAA GCA
    ---
      172      181      190      199      208      217
    GCT GGA GTG CGA CCG CCA CGG CAG CCA CCC TGC AAC CGC CAG TCG GAG GTG CAG
    ---
      226      235      244      253      262      271
    TCC GTA GGC CCT GGC CCC CGG GTG GGC CCT TGG GGA GTC GGC GCC GCT CCC GAG
    ---
      280      289      298      307      316      325
    GAG CTG CAA GGC TCG CCC CTG CCC GGC GTG GAG GGC GCG GGG GGC GCG GAG GAT
    ---
      334      343      352      361      370      379
    ATT CTT GGT GAT CTT GGA AGT GTC CGT ATC ATG GAA TCA ATC TCT ATG ATG GGA
    ---

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(SEQ ID NO:6) → M E S I S M M G

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      388      397      406      415      424      433
    AGC CCT AAG AGC CTT AGT GAA ACT TGT TTA CCT AAT GGC ATA AAT GGT ATC AAA
    ---
    S   P   K   S   L   S   E   T   C   L   P   N   G   I   N   G   I   K

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      442      451      460      469      478      487
    GAT GCA AGG AAG GTC ACT GTA GGT GTG ATT GGA AGT GGA GAT TTT GCC AAA TCC
    ---
    D   A   R   K   V   T   V   G   V   I   G   S   G   D   F   A   K   S

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      496      505      514      523      532      541
    TTG ACC ATT CGA CTT ATT AGA TGC GGC TAT CAT GTG GTC ATA GGA AGT AGA AAT
    ---
    L   T   I   R   L   I   R   C   G   Y   H   V   V   I   G   S   R   N

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      550      559      568      577      586      595
    CCT AAG TTT GCT TCT GAA TTT TTT CCT CAT GTG GTA GAT GTC ACT CAT CAT GAA
    ---
    P   K   F   A   S   E   F   F   P   H   V   V   D   V   T   H   H   E

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      604      613      622      631      640      649
    GAT GCT CTC ACA AAA ACA AAT ATA ATA TTT GTT GCT ATA CAC AGA GAA CAT TAT
    ---
    D   A   L   T   K   T   N   I   I   F   V   A   I   H   R   E   H   Y

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      658      667      676      685      694      703
    ACC TCC CTG TGG GAC CTG AGA CAT CTG CTT GTG GGT AAA ATC CTG ATT GAT GTG
    ---
    T   S   L   W   D   L   R   H   L   L   V   G   K   I   L   I   D   V

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      712      721      730      739      748      757
    AGC AAT AAC ATG AGG ATA AAC CAG TAC CCA GAA TCC AAT GCT GAA TAT TTG GCT
    ---
    S   N   N   M   R   I   N   Q   Y   P   E   S   N   A   E   Y   L   A

```

766 775 784 793 802 811
TCA TTA TTC CCA GAT TCT TTG ATT GTC AAA GGA TTT AAT GTT GTC TCA GCT TGG
S L F P D S L I V K G F N V V S A W

820 829 838 847 856 865
GCA CTT CAG TTA GGA CCT AAG GAT GCC AGC CGG CAG GTT TAT ATA TGC AGC AAC
A L Q L G P K D A S R Q V Y I C S N

874 883 892 901 910 919
AAT ATT CAA GCG CGA CAA CAG GTT ATT GAA CTT GCC CGC CAG TTG AAT TTC ATT
N I Q A R Q Q V I E L A R Q L N F I

928 937 946 955 964 973
CCC ATT GAC TTG GGA TCC TTA TCA TCA GCC AGA GAG ATT GAA AAT TTA CCC CTA
P I D L G S L S S A R E I E N L P L

982 991 1000 1009 1018 1027
CGA CTC TTT ACT CTC TGG AGA GGG CCA GTG GTG GTA GCT ATA AGC TTG GCC ACA
R L F T L W R G P V V V A I S L A T

1036 1045 1054 1063 1072 1081
TTT TTT TTC CTT TAT TCC TTT GTC AGA GAT GTG ATT CAT CCA TAT GCT AGA AAC
F F F L Y S F V R D V I H P Y A R N

1090 1099 1108 1117 1126 1135
CAA CAG AGT GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT
Q Q S D F Y K I P I E I V N K T L P

1144 1153 1162 1171 1180 1189
ATA GTT GCC ATT ACT TTG CTC TCC CTA GTA TAC CTT GCA GGT CTT CTG GCA GCT
I V A I T L L S L V Y L A G L L A A

1198 1207 1216 1225 1234 1243
GCT TAT CAA CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA
A Y Q L Y Y G T K Y R R F P P W L E

1252 1261 1270 1279 1288 1297
ACC TGG TTA CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG
T W L Q C R K Q L G L L S F F F A M

1306 1315 1324 1333 1342 1351
GTC CAT GTT GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG
V H V A Y S L C L P M R R S E R Y L

1360 1369 1378 1387 1396 1405
TTT CTC AAC ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT
F L N M A Y Q Q V H A N I E N S W N

1414 1423 1432 1441 1450 1459
GAG GAA GAA GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT
E E E V W R I E M Y I S F G I M S L

FIG. 9B

1468	1477	1486	1495	1504	1513
GGC TTA CTT TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GAG AGC AAT GCT TTA					
G L L S L L A V T S I P S V S N A L					
1522	1531	1540	1549	1558	1567
AAC TGG AGA GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC					
N W R E F S F I Q S T L G Y V A L L					
1576	1585	1594	1603	1612	1621
ATA AGT ACT TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT TTT GAG GAA GAG					
I S T F H V L I Y G W K R A F E E E					
1630	1639	1648	1657	1666	1675
TAC TAC AGA TTT TAT ACA CCA CCA AAC TTT GTT CTT GCT CTT GTT TTG CCC TCA					
Y Y R F Y T P P N F V L A L V L P S					
1684	1693	1702	1711	1720	1729
ATT GTA ATT CTG GAT CTT TTG CAG CTT TGC AGA TAC CCA GAC TGA GCT GGA ACT					
I V I L D L L Q L C R Y P D *					
1738	1747	1756	1765	1774	1783
GGA ATT TGT CTT CCT ATT GAC TCT ACT TCT TTA AAA GCG GCT GCC CAT TAC ATT					
1792	1801	1810	1819	1828	1837
CCT CAG CTG TCC TTG CAG TTA GGT GTA CAT GTG ACT GAG TGT TGG CCA GTG AGA					
1846	1855	1864	1873	1882	1891
TGA AGT CTC CTC AAA GGA AGG CAG CAT GTG TCC TTT TTC ATC CCT TCA TCT TGC					
1900	1909	1918	1927	1936	1945
TGC TGG GAT TGT GGA TAT AAC AGG AGC CCT GGC AGC TGT CTC CAG AGG ATC AAA					
1954	1963	1972	1981	1990	1999
GCC ACA CCC AAA GAG TAA GGC AGA TTA GAG ACC AGA AAG ACC TTG ACT ACT TCC					
2008	2017	2026	2035	2044	2053
CTA CTT CCA CTG CTT TTC CTG CAT TTA AGC CAT TGT AAA TCT GGG TGT GTT ACA					
2062	2071	2080	2089	2098	2107
TGA AGT GAA AAT TAA TTC TTT CTG CCC TTC AGT TCT TTA TCC TGA TAC CAT TTA					
2116	2125	2134	2143	2152	2161
ACA CTG TCT GAA TTA ACT AGA CTG CAA TAA TTC TTT CTT TTG AAA GCT TTT AAA					
2170	2179	2188	2197	2206	2215
GGA TAA TGT GCA ATT CAC ATT AAA ATT GAT TTT CCA TTG TCA ATT AGT TAT ACT					
2224	2233	2242	2251	2260	2269
CAT TTT CCT GCC TTG ATC TTT CAT TAG ATA TTT TGT ATC TGC TTG GAA TAT ATT					
2278	2287	2296	2305	2314	2323
ATC TTC TTT TTA ACT GTG TAA TTG GTA ATT ACT AAA ACT CTG TAA TCT CCA AAA					
2332	2341	2350	2359	2368	2377
TAT TGC TAT CAA ATT ACA CAC CAT GTT TTC TAT CAT TCT CAT AGA TCT GCC TTA					
2386	2395	2404	2413	2422	2431
TAA ACA TTT AAA TAA AAA GTA CTA TTT AAT GAT TTA AAA AAA AAA AAA AAA AAA					
2440	2449				
AAA AAA AAA AAA AAA AAA AAA AA 3'					

FIG. 9C

FIG. 10A-1

(SEQ ID NO:7)

1 CGAAACTTCC CTCTACCCGC CCGGCCCCGC GCGCGCACCG TTGGCGCTGG ACGCTTCCTC
GCTTTGAAGG GAGATGGGCG GGCCGGGCGC CGCGCGTGGC AACC GCGACC TGCGAAGGAG

(SEQ ID NO:8) → M E K T C I D A L P L T

61 CTTGGAAGCG CCTCTCCCTC AGTTATGGAG AAAACTTGTA TAGATGCACT TCCTCTTACT
GAACCTTCGC GGAGAGGGAG TCAATACCTC TTTTGAACAT ATCTACGTGA AGGAGAATGA

M N S S E K Q E T V C I F G T G D F G R
121 ATGAATTCTT CAGAAAAGCA AGAGACTGTA TGTATTTTTG GAACTGGTGA TTTTGAAGA
TACTTAAGAA GTCTTTTCGT TCTCTGACAT ACATAAAAAC CTTGACCACT AAAACCTTCT

S L G L K M L Q C G Y S V V F G S R N P
181 TCACTGGGAT TGAAAATGCT CCAGTGTGGT TATTCTGTTG TTTTGGGAAG TCGAAACCCC
AGTGACCCTA ACTTTTACGA GGTCACACCA ATAAGACAAC AAAAACCTTC AGCTTTGGGG

Q K T T L L P S G A E V L S Y S E A A K
241 CAGAAGACCA CCCTACTGCC CAGTGGTGCA GAAGTCTTGA GCTATTCAGA AGCAGCCAAG
GTCTTCTGGT GGGATGACGG GTCACCACGT CTTCAGAACT CGATAAGTCT TCGTCGGTTC

K S G I I I I A I H R E H Y D F L T E L
301 AAGTCTGGCA TCATAATCAT AGCAATCCAC AGAGAGCATT ATGATTTTCT CACAGAATTA
- TTCAGACCGT AGTATTAGTA TCGTTAGGTG TCTCTCGTAA TACTAAAAGA GTGTCTTAAT

T E V L N G K I L V D I S N N L K I N Q
361 ACTGAGGTTT TCAATGGAAA AATATTGGTA GACATCAGCA ACAACCTCAA AATCAATCAA
TGACTCCAAG AGTTACCTTT TTATAACCAT CTGTAGTCGT TGTTGGAGTT TTAGTTAGTT

Y P E S N A E Y L A H L V P G A H V V K
421 TATCCAGAAT CTAATGCAGA GTACCTTGCT CATTTGGTGC CAGGAGCCCA CGTGGTAAAA
ATAGGTCTTA GATTACGTCT CATGGAACGA GTAAACCACG GTCCTCGGGT GCACCATTTT

A F N T I S A W A L Q S G A L D A S R Q
481 GCATTTAACA CCATCTCAGC CTGGGCTCTC CAGTCAGGAG CACTGGATGC AAGTCGGCAG
CGTAAATTGT GGTAGAGTCG GACCCGAGAG GTCAGTCCTC GTGACCTACG TTCAGCCGTC

V F V C G N D S K A K Q R V M D I V R N
541 GTGTTTGTGT GTGGAAATGA CAGCAAAGCC AAGCAAAGAG TGATGGATAT TGTTCGTAAT
CACAAACACA CACCTTTACT GTCGTTTCGG TTCGTTTCTC ACTACCTATA ACAAGCATTA

L G L T P M D Q G S L M A A K E I E K Y
601 CTTGGACTTA CTCCAATGGA TCAAGGATCA CTCATGGCAG CCAAAGAAAT TGAAAAGTAC
GAACCTGAAT GAGGTTACCT AGTTCCTAGT GAGTACCGTC GGTTTCTTTA ACTTTTCATG

P L Q L F P M W R F P F Y L S A V L C V
661 CCCCTGCAGC TATTTCCAAT GTGGAGGTTT CCCTTCTATT TGTCTGCTGT GCTGTGTGTC
GGGGACGTCG ATAAAGGTTA CACCTCCAAG GGGAAAGATAA ACAGACGACA CGACACACAG

F L F F Y C V I R D V I Y P Y V Y E K K
721 TTCTTGTTTT TCTATTGTGT TATAAGAGAC GTAATCTACC CTTATGTTTA TGAAAAGAAA
AAGAACAAAA AGATAACACA ATATTCTCTG CATTAGATGG GAATACAAAT ACTTTTCTTT

D N T F R M A I S I P N R I F P I T A L
 781 GATAATACAT TTCGTATGGC TATTTCCATT CCAAATCGTA TCTTTCCAAT AACAGCACTT
 CTATTATGTA AAGCATACCG ATAAAGGTAA GGTTTAGCAT AGAAAGGTGA TTGTCGTGAA

 T L L A L V Y L P G V I A A I L Q L Y R
 841 AACTGCTTG CTTTGGTTTA CCTCCCTGGT GTTATTGCTG CCATTCTACA ACTGTACCGA
 TGTGACGAAC GAAACCAAAT GGAGGGACCA CAATAACGAC GGTAAGATGT TGACATGGCT

 G T K Y R R F P D W L D H W M L C R K Q
 901 GGCACAAAAT ACCGTCGATT CCCAGACTGG CTTGACCACT GGATGCTTTG CCGAAAGCAG
 CCGTGTTTTA TGGCAGCTAA GGGTCTGACC GAACTGGTGA CCTACGAAAC GGCTTTCTGT

 L G L V A L G F A F L H V L Y T L V I P
 961 CTTGGCTTGG TAGCTCTGGG ATTTGCCTTC CTTTCATGTCC TCTACACACT TGTGATTCTT
 GAACCGAACC ATCGAGACCC TAAACGGAAG GAAGTACAGG AGATGTGTGA AACTAAGGA

 I R Y Y V R W R L G N L T V T Q A I L K
 1021 ATTCGATATT ATGTACGATG GAGATTGGGA AACTTAACCG TTACCCAGGC AATACTCAAG
 TAAGCTATAA TACATGCTAC CTCTAACCTT TTGAATTGGC AATGGGTCCG TTATGAGTTC

 K E N P F S T S S A W L S D S Y V A L G
 1081 AAGGAGAATC CATTAGCAC CTCCTCAGCC TGGCTCAGTG ATTCATATGT GGCTTTGGGA
 TTCCTCTTAG GTAAATCGTG GAGGAGTCGG ACCGAGTCAC TAAGTATACA CCGAAACCTT

 I L G F F L F V L L G I T S L P S V S N
 1141 ATACTTGGGT TTTTCTGTG TGTACTCTTG GGAATCACTT CTTTGCCATC TGTTAGCAAT
 TATGAACCCA AAAAAGACAA ACATGAGAAC CCTTAGTGAA GAAACGGTAG ACAATCGTTA

 A V N W R E F R F V Q S K L G Y L T L I
 1201 GCAGTCAACT GGAGAGAGTT CCGATTTGTC CAGTCCAAAC TGGGTATTTT GACCCTGATC
 CGTCAGTTGA CCTCTCTCAA GGCTAAACAG GTCAGGTTTG ACCCAATAAA CTGGGACTAG

 L C T A H T L V Y G G K R F L S P S N L
 1261 TTGTGTACAG CCCACACCCT GGTGTACGGT GGGAAAGAGAT TCCTCAGCCC TTCAAATCTC
 AACACATGTC GGGTGTGGGA CCACATGCCA CCCTTCTCTA AGGAGTCGGG AAGTTTAGAG

 R W Y L P A A Y V L G L I I P C T V L V
 1321 AGATGGTATC TTCCTGCAGC CTACGTGTGA GGGCTTATCA TTCCTTGCAC TGTGCTGGTG
 TCTACCATAG AAGGACGTCG GATGCACAAT CCCGAATAGT AAGGAACGTG ACACGACCAC

 I K F V L I M P C V D N T L T R I R Q G
 1381 ATCAAGTTTG TCCTAATCAT GCCATGTGTA GACAACACCC TTACAAGGAT CCGCCAGGGC
 TAGTTCAAAC AGGATTAGTA CGGTACACAT CTGTTGTGGG AATGTTCTTA GGCGGTCCCC

 W E R N S K H
 1441 TGGGAAAGGA ACTCAAAACA CTAGAAAAG CATTGAATGG AAAATCAATA TTTAAACAA
 ACCCTTTCCT TGAGTTTTGT GATCTTTTTC GTAACCTACC TTTTAGTTAT AAATTTTGTT

 1501 AGTTCAATTT AGCTGGATTT CTGAACTATG GTTTTGAATG TTTAAAGAAG AATGATGGGT
 TCAAGTTAAA TCGACCTAAA GACTTGATAC CAAAACCTAC AAATTTCTTC TTACTACCCA

 1561 ACAGTTAGGA AAGTTTTTTT CTTACACCGT GACTGAGGGA AACATTGCTT GTCTTTGAGA
 TGTCAATCCT TTCAAAAAAA GAATGTGGCA CTGACTCCCT TTGTAACGAA CAGAAACTCT

 1621 AATTGACTGA CATACTGGAA GAGAACACCA TTTTATCTCA GGTTAGTGAA GAATCAGTGC
 TTAAGTACT GTATGACCTT CTCTTGTGGT AAAATAGAGT CCAATCACTT CTTAGTCACG

FIG. 10A-2

1681 AGGTCCCTGA C...TTATTTT CCCAGAGGCC ATGGAGCTGA G...TGAGACT AGCCTTGTGG
 TCCAGGGACT GAGAATAAAA GGGTCTCCGG TACCTCGACT CTAACTCTGA TCGGAACACC
 1741 TTTCACACTA AAGAGTTTCC TTGTTATGGG CAACATGCAT GACCTAATGT CTTGCAAAAT
 AAAGTGTGAT TTCTCAAAGG AACAATACCC GTTGTACGTA CTGGATTACA GAACGTTTAA
 1801 CCAATAGAAG TATTGCAGCT TCCTTCTCTG GCTCAAGGGC TGAGTTAAGT GAAAGGAAAA
 GGTATCTTC ATAACGTCGA AGGAAGAGAC CGAGTTCCCG ACTCAATTCA CTTTCCTTTT
 1861 ACAGCACAAT GGTGACCACT GATAAAGGCT TTATTAGGTA TATCTGAGGA AGTGGGTCAC
 TGTCGTGTTA CCACTGGTGA CTATTTCCGA AATAATCCAT ATAGACTCCT TCACCCAGTG
 1921 ATGAAATGTA AAAAGGGAAT GAGGTTTTTG TTGTTTTTTG GAAGTAAAGG CAAACATAAA
 TACTTTACAT TTTTCCCTTA CTCCAAAAAC AACAAAAAAC CTTCATTTCC GTTTGTATTT
 1981 TATTACCATG ATGAATTCTA GTGAAATGAC CCCTTGACTT TGCTTTTCTT AATACAGATA
 ATAATGGTAC TACTTAAGAT CACTTTACTG GGGAACTGAA ACGAAAAGAA TTATGTCTAT
 2041 TTTACTGAGA GGAACATTTT TTATAACACA AGAAAAATTT ACAATTGATT AAAAGTATCC
 AAATGACTCT CCTTGATAAA AATATTGTGT TCTTTTAA TGTAACTAA TTTTCATAGG
 2101 ATGTCTTGGA TACATACGTA TCTATAGAGC TGGCATGTAA TTCTTCCTCT ATAAAGAATA
 TACAGAACCT ATGTATGCAT AGATATCTCG ACCGTACATT AAGAAGGAGA TATTTCTTAT
 2161 GGTATAGGAA AGACTGAATA AAAATGGAGG GATATCCCCT TGGATTTTAC TTGCATTGTG
 CCATATCCTT TCTGACTTAT TTTTACCTCC CTATAGGGGA ACCTAAAGTG AACGTAACAC
 2221 CAATAAGCAA AGAAGGGTTG ATAAAAGTTC TTGATCAAAA AGTTCAAAGA AACCAGAATT
 GTTATTCGTT TCTTCCAAC TATTTTCAAG AACTAGTTT TCAAGTTTCT TTGGTCTTAA
 2281 TTAGACAGCA AGCTAAATAA ATATTGTAAA ATTGCACTAT ATTAGGTAA GTATTATTTA
 AATCTGTCGT TCGATTAT TATAACATTT TAACGTGATA TAATCCAATT CATAATAAAT
 2341 GGTATTATAA TATGCTTTGT AAATTTTATA TTCCAAATAT TGCTCAATAT TTTTCATCTA
 CCATAATATT ATACGAAACA TTTAAATAT AAGGTTTATA ACGAGTTATA AAAAGTAGAT
 2401 TTAAATTAAT TTCTAGTGTA AATAAGTAGC TTCTATATCT GTCTTAGTCT ATTATAATTG
 AATTTAATTA AAGATCACAT TTATTCATCG AAGATATAGA CAGAATCAGA TAATATTAAC
 2461 TAAGGAGTAA AATTAAATGA ATAGTCTGCA GGTATAAATT TGAACAATGC ATAGATGATC
 ATCCTCATT TTAATTTACT TATCAGACGT CCATATTTAA ACTTGTTACG TATCTACTAG
 2521 GAAAATTACG GAAAATCATA GGCAGAGAG GTGTGAAGAT TCATCATTAT GTGAAATTTG
 CTTTAAATGC CTTTGTAGTAT CCCGTCTCTC CACACTTCTA AGTAGTAATA CACTTTAAAC
 2581 GATCTTTCTC AAATCCTTGC TGAAATTTAG GATGGTTCTC ACTGTTTTTC TGTGCTGATA
 CTAGAAAGAG TTTAGGAACG ACTTTAAATC CTACCAAGAG TGACAAAAAG ACACGACTAT
 2641 GTACCCTTTC CAAGGTGACC TTCAGGGGGA TTAACCTTCC TAGCTCAAGC AATGAGCTAA
 CATGGGAAAG GTTCCACTGG AAGTCCCCCT AATTGGAAGG ATCGAGTTCG TTACTCGATT
 2701 AAGGAGCCTT ATGCATGATC TTCCACATA TCAAAATAAC TAAAAGGCAC TGAGTTTGGC
 TTCTTCGGAA TACGTACTAG AAGGGTGTAT AGTTTTATTG ATTTCCGTG ACTCAAACCG
 2761 ATTTTCTGCT CTGCTCTGCT AAGACCTTTT TTTTTTTTTT ACTTTCATTA TAACATATTA
 TAAAAAGACG GACGAGACGA TTCTGGAAAA AAAAAAAAAA TGAAAGTAAT ATTGTATAAT

FIG. 10A-3

2821 TACATGACAT T. AAAAAA TGATTAAAAT ATATTAAAAC A. ATCAACA ATCCAGGATA
 ATGTA CTGTA ATATGTTTTT ACTAATTTTA TATAATTTTG TTGTAGTTGT TAGGTCCTAT
 2881 TTTTCTATA AAAC TTTTAA AAAATAATTG TATCTATATA TTCAATTTTA CATCCTTTTT
 AAAAAAGATAT TTGAAAAAT TTTTATTAAC ATAGATATAT AAGTTAAAAT GTAGGAAAAA
 2941 CAAAGGCTTT GTTTTTCTAA AGGCTTTGTT TTCCTTTTTA TTATTTTTTT CTTTTTTATT
 GTTTCGAAA CAAAAAGATT TCCGAAACAA AAGGAAAAAT AATAAAAAAA GAAAAATAA
 3001 TTTTGTAGAC AGTCTTGCTC TGTCGCTCAG GCTGGAGTGC AGTGGCACGA TCTCAGCTCA
 AAAAACTCTG TCAGAACGAG ACAGCGAGTC CGACCTCACG TCACCGTGCT AGAGTCGAGT
 3061 CTGCAACCTC CTCCTCCCAG GTTCAAGTGA TTCTTGTTCA TCAGCCTCCC GAGTAGCTGG
 GACGTTGGAG GAGGAGGGTC CAAGTTCAC TAAACAAGT AGTCGGAGGG CTCATCGACC
 3121 GACTACAGGC ATGTGCCACT ATGCCAGCT AATTTTGTGA CTTTGTAGTAG AGACAGGGTT
 CTGATGTCCG TACACGGTGA TACGGGTCGA TAAAAACAT GAAATCATC TCTGTCCCAA
 3181 TCACCACATT GGTCAGGCTG GTCTTGAAAT GCTGGCGTCA AGTGATCTGC CTGCCTCCGC
 AGTGGTGTA CCAGTCCGAC CAGAACTTTA CGACCGCAGT TCACTAGACG GACGGAGGCG
 3241 CTTACGTAAT ATATTTTCTT AATGGCTGCA TAATATCACA TCAAATAGGC ATTTTCAAA
 GAATGCATTA TATAAAGAA TTACCGACGT ATTATAGTGT AGTTTATCCG TAAAAAGTTT
 3301 CCTCTTTCCT TATTAAACAT GTAGACTATA TCCATTTTTT ACTAAAATAA ATAACATTC
 GGAGAAAGGA ATAATTTGTA CATCTGATAT AGGTAAAAAA TGATTTTATT TATTGTAAAG
 3361 AGATAATATC TTTGCACTGA TAATGTTGCC AAGCCATTTT TAAAGTGACC TTATCAATTT
 TCTATTATAG AAACGTGACT ATTACAACGG TTCGGTAAAG ATTTCACTGG AATAGTTAAA
 3421 AATTACCATT GGATGAGGGT GTTGCTTTCA TCGCACCATT GTAGATTGTC TTTTTATTT
 TTAATGGTAA CCTACTCCCA CAACGAAAGT AGCGTGGTAA CATCTAACAG AAAAAATAAA
 3481 CAATTTGCGT TTATTTATAA CTGGTTGCAA AGGTACACAG AACACACGCT CCTTCAACTT
 GTTAAACGCA AATAAATATT GACCAACGTT TCCATGTGTC TTGTGTGCGA GGAAGTTGAA
 3541 ATCTTTGATA AACCCAAGCA AGGATACAAA AAGTTGGACG ACATTGAGTA GAGTCATGGT
 TAGAACTAT TTGGGTTTCGT TCCTATGTTT TTCAACCTGC TGTAACCTCAT CTCAGTACCA
 3601 ATACGGTGCT GACCCTACAG TATCAGTGGA AAAGATAAGG AAAATGTCAC TACTCACCTA
 TATGCCACGA CTGGGATGTC ATAGTCACCT TTTCTATTCC TTTTACAGTG ATGAGTGGAT
 3661 TGTTATGCAA AACAGTTAGG TGTGCTGGGG CTGGATACTG CTCTTTTACT TGAGCATTGG
 ACAATACGTT TTGTCAATCC ACACGACCCC GACCTATGAC GAGAAAATGA ACTCGTAACC
 3721 TTGATTAAAG TTTAGGTACC ATCCAGGCTG GTCTAGAGAA GTCTTTGGAG TTAACCATGC
 AACTAATTTT AAATCCATGG TAGGTCCGAC CAGATCTCTT CAGAAACCTC AATTGGTACG
 3781 TCTTTTTGTT AAAGAAGAGA GTAATGTGTT TATCCTGGCT CATAGTCCGT CACCGAAAAT
 AGAAAAACAA TTTCTTCTCT CATTACACAA ATAGGACCGA GTATCAGGCA GTGGCTTTTA
 3841 AGAAAATGCC ATCCATAGGT AAAATGCTGA CCTATAGAAA AAAATGAACT CACTTTTAT
 TCTTTTACGG TAGGTATCCA TTTTACGACT GGATATCTTT TTTTACTTGA GATGAAAATA
 3901 AGCCTAGTAA AAATGCTCTA CCTGAGTAGT TAAAAGCAAT TCATGAAGCC TGAAGCTAAA
 TCGGATCATT TTTACGAGAT GGACTCATCA ATTTTCGTGA AGTACTTCGG ACTTCGATTT

FIG. 10A-4

3961 GAGCACTCTG A. JTTTTGG CATAATAGCT GCATTTCCAG A. TGACCTT TGGCCCCAAC
 CTCGTGAGAC TACCAAACC GTATTATCGA CGTAAAGGTC TGGACTGGAA ACCGGGGTTG
 4021 CACAAGTGCT CCAAGCCCCA CCAGCTGACC AAAGAAAGCC CAAGTTCTCC TTCTGTCCTT
 GTGTTACGA GGTTCGGGT GGTGACTGG TTTCTTTCGG GTTCAAGAGG AAGACAGGAA
 4081 CCCACAACCT CCCTGCTCCC AAAACTATGA AATTAATTTG ACCATATTAA CACAGCTGAC
 GGGTGTGGA GGGACGAGG TTTGATACT TTAATTAAAC TGGTATAATT GTGTCGACTG
 4141 TCCTCCAGTT TACTTAAGGT AGAAAGAATG AGTTTACAAC AGATGAAAAT AAGTGCTTTG
 AGGAGGTCAA ATGAATTCCA TCTTCTTAC TCAAATGTTG TCTACTTTTA TTCACGAAAC
 4201 GGCGAACTGT ATTCCTTTTA ACAGATCCAA ACTATTTTAC ATTTAAAAAA AAAGTTAAAC
 CCGCTTGACA TAAGGAAAAT TGTCTAGGTT TGATAAAATG TAAATTTTTT TTTCAATTTG
 4261 TAAACTTCTT TACTGCTGAT ATGTTTCCTG TATTCTAGAA AAATTTTAC ACTTTCACAT
 ATTTGAAGAA ATGACGACTA TACAAAGGAC ATAAGATCTT TTTAAAAATG TGAAAGTGTA
 4321 TATTTTTGTA CACTTTCCCC ATGTTAAGGG ATGATGGCTT TTATAAATGT GTATTCATTA
 ATAAAAACAT GTGAAAGGGG TACAATTCCC TACTACCGAA AATATTTACA CATAAGTAAT
 4381 AATGTTACTT TAAAAATAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
 TTACAATGAA ATTTTTATTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

FIG. 10A-5

FIG. 10B

STEAP-2, AA508880 (NCI_CGAP Pr6)

ggtcgacttttccctttattcctttgtcagagatctgattcatccatgctagaaaccaacagagtgactttttaca
aaattcctatagagattgtgaataaaaaccttacctatagttgccattactttgctctccctagtataccttgcagg
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttggttggaacctgggta
cagtgtagaaaacagcttggattactaagttgtttcttcgctatggtccatggtgcctacagcctctgcttaccga
tgagaaggctcagagagat (SEQ ID NO:9)

STEAP-2, 98P4B6 SSH fragment

TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAAGTGAATTGTCTTCCTATTGACTCTACTTCTTTAAAGCG
GCTGCCCATTACATTCCTCAGCTGTCTTGCAGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGTCCTTTTT (SEQ ID NO:10)

STEAP-3, AI139607 (testis EST)

aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaataacttgggtttt
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcaactggagagagttccgatttgt
ccagtcctaaactgggttatttgacctgatcttgtgtacagccacaccctggtgtacggtgggaagagattcctc
agcccttcaaactctcagatggtatcttctcgcagcctacgtgttagggcttatcattccttgcactgtgctgggta
tcaagtttgcctaatcatgccatgtgtagacaacacccttacaaggatccgccagggtgggaaggaactcaa
acactagaaaaagcattgaatggaaaatcaatatttaaaacaaagttcaatttagctggaaaaaaaaa

(SEQ ID NO:11)

STEAP 4, R80991 (placental EST)

ggccgcggcanccgctacgacctggtcaacctggcagtcgaagcaggtcttggccanacaagagccacctctgggtg
aaggaggaggtctggcggatggagatctacctctccctgggagtgctggccctcggcacgttgtccctgctggccg
tgacctcactgcccgtccattgcaaactcgtcaactggaggaggttcagcttcgttcagtcctcactgggctttgt
ggcctcgtgctgagcacactncacacgctcacctacggctggaccgcgccttcgaggagagccgctacaagttc
tacctnctcccaccttcacgntcacgctgctgggtgccctgcgttcggttcacctcctgggcaaaagccctgtttntac
tgcttgcattcagccgnaga (SEQ ID NO:12)

FIG. 11A-1

[illegible]

361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871
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	451	465	466	480	481
2	STEAP2	LLQICRYED			
3	STEAP3	FVILPGDNTLTR	QGVERNSKH		454
4	STEAP1	SILFLGRLKKILK	RHGVEDVTK		459
5	STEAP4	AKAIFXLCIQPX			339
					133

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STRAP-1      67 LFPQWHLPIKIAAIIASLTFLYTLTREVHPLATSHQQYFYKIPILVINKVLPMSITLL
STRAP-2     208 LFTLWRGFPVVVAISLATFFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLL
          ** * * * * * ** * * * * * * * * * * *
STRAP-1     127 ALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWLTRKQFGLLSFFFVAVLHAIYSLSPMRR
STRAP-2     268 SLVYLAGLLAAAYQLYYGTKYRRFPWLETWLQCRKQLGLLSFFFAMVHVAYSCLCLPMRR
          **** * ** ** * * * * * * * * * * * * * * *
STRAP-1     187 SYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSLT
STRAP-2     328 SERYLEFLNMAYQQVHANIEANSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALN
          * * * ** * * * * * * * * * * * * * * * * *
STRAP-1     247 WREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVLI
STRAP-2     388 WREFSFIQSTLGIYVALLISTFEVLIYGWKRAFEEEYRYFTPPNFVALVLPISIVL
          **** * * * * * * * * * * * * * * * * *

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FIG. 11C

STEAP1 66 ELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMSITL

STEAP3 195 QLFPMWRFPPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTL
* * * * *

STEAP1 126 LALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFVAVLHAIYSLSPMR

STEAP3 255 LALVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIR
* * * * *

STEAP1 186 RSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSL

STEAP3 315 YYVRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFVLLGITSLSVSNV
* * * * *

STEAP1 246 TWREFHYIQSKLGIVSLLLGTHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLIFK

STEAP3 375 NWREFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAAYVLGLIIPCTVLVIK
* * * * *

STEAP1 306 SILFLPCLRKKILKIRHWEDVTK

STEAP3 435 FVLIMPCVDNTLTRIRQGWERNK
* * * * *

FIG. 11D

STEAP2 29 RKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHEDALTKTNI

STEAP3 18 KQETVCIFGTGDFGRSLGLKMLQCGYSVVFGSRNPQ-KTTLLPSGAEVLSYSEAAKSGI
 ** * *** ** **** * * * *

STEAP2 89 IFVAIHREHYTSLWDLRHLLVGKILIDVSNMNRINQYPESNAEYLAFLPDSLIVKGFNV

STEAP3 77 IIIIAIHREHYDFLTEVLNGKILVDISNNLKINQYPESNAEYLAHLVPGAHVVKAFNT
 * ***** * * * ***** * * ** *

STEAP2 149 VSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDLGLSSAREIENLPLRL

STEAP3 137 ISAWALQSGALDASRQVFVCGNSKAKQVRMDIVRNGLTPMDQGSMAAKEIEKYPLQL
 ***** * ***** * * * * * * * * * * * * *

STEAP2 209 FTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLLS

STEAP3 197 FPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTLA
 * * * * * * * * * * * * * * * * *

STEAP2 269 LVYLAGLLAAAYQLYYGTKYRRFPWLETWLQCRKQLGLLSFFFAMVHVAYSCLPMRRS

STEAP3 257 LVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIRYY
 ***** * * * * * * * * * * * * * * * * *

STEAP2 329 ERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNW

STEAP3 317 VRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLVLLGITSLSVSNVNW
 * * * * * * * * * * * * * * * * *

STEAP2 389 REFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYRYFTPPNFVLALVLPISIVIL

STEAP3 377 REFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAVYVGLIIPCTVLV
 *** * * * * * * * * * * * * * * * *

FIG. 1A-1

(SEQ ID NO:1)

5' 11 20 29 38 47 56
 GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT

 65 74 83 92 101 110
 ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA

 (SEQ ID NO:2) M E S R K D I T N Q E E L W K

 119 128 137 146 155 164
 ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA

 M K P R R N L E E D D Y L H K D T G

 173 182 191 200 209 218
 GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT

 E T S M L K R P V L L H L H Q T A H

 227 236 245 254 263 272
 GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA

 A D E F D C P S E L Q H T Q E L F P

 281 290 299 308 317 326
 CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT

Q W H L P I K I A A I I A S L T F L

 335 344 353 362 371 380
 TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT

Y T L L R E V I H P L A T S H Q Q Y

 389 398 407 416 425 434
 TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC

 F Y K I P I L V I N K V L P M V S I

 443 452 461 470 479 488
 ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT

T L L A L V Y L P G V I A A I V Q L

 497 506 515 524 533 542
 CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA

 H N G T K Y K K F P H W L D K W M L

 551 560 569 578 587 596
 ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT

 T R K Q F G L L S F F F A V L H A I

 605 614 623 632 641 650
 TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG

Y S L S Y P M R R S Y R Y K L L N W

FIG. 1A-2

3. 1A - SHEET 2 OF 2

659	668	677	686	695	704
GCA TAT CAA CAG GTC	CAA CAA AAT AAA	GAA GAT GCC TGG	ATT GAG CAT GAT	GTT	
A Y Q Q V	Q Q N K E D	A W I E H D	V		
713	722	731	740	749	758
TGG AGA ATG GAG ATT	TAT GTG TCT CTG	GGA ATT GTG GGA	TTG GCA ATA CTG	GCT	
W R M E I	Y V S L G I V	G L A I L A			
767	776	785	794	803	812
CTG TTG GCT GTG ACA TCT	ATT CCA TCT GTG AGT	GAC TCT TTG ACA TGG	AGA GAA		
L L A V T S I P S V	S D S L T W R E				
821	830	839	848	857	866
TTT CAC TAT ATT CAG AGC	AAG CTA GGA ATT GTT	TCC CTT CTA CTG GGC	ACA ATA		
F H Y I Q	S K L G I V S	L L L G T I			
875	884	893	902	911	920
CAC GCA TTG ATT TTT GCC	TGG AAT AAG TGG ATA	GAT ATA AAA CAA	TTT GTA TGG		
H A L I F A W N K	W I D I K Q F V W				
929	938	947	956	965	974
TAT ACA CCT CCA ACT TTT	ATG ATA GCT GTT TTC	CTT CCA ATT GTT	GTC CTG ATA		
Y T P P T F	M I A V F L P I V V L I				
983	992	1001	1010	1019	1028
TTT AAA AGC ATA CTA TTC	CTG CCA TGC TTG AGG	AAG AAG ATA CTG	AAG ATT AGA		
F K S I L F L P C L	R K K I L K I R				
1037	1046	1055	1064	1073	1082
CAT GGT TGG GAA GAC GTC	ACC AAA ATT AAC AAA	ACT GAG ATA TGT	TCC CAG TTG		
H G W E D V T K I N K T	E I C S Q L				
1091	1100	1109	1118	1127	1136
TAG AAT TAC TGT TTA CAC	ACA TTT TTG TTC AAT	ATT GAT ATA TTT	TAT CAC CAA		
* N Y C L H T F L F N I D I F Y H Q					
1145	1154	1163	1172	1181	1190
CAT TTC AAG TTT GTA TTT	GTT AAT AAA ATG ATT	ATT CAA GGA AAA	AAA AAA AAA		
H F K F V F V N K M I I Q G K K K K					

AAA AA 3'

K

FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3' (SEQ ID NO: 3)

FIG. 4A

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC
ATACTATTTTATAGAATTAATGGAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG
AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACCTCTTCCACA
GTGGCACTTGCCAAATAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATT
CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCGAATCCTGGTCATCAACAAAGTCTTGCCAAATGG
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTTCATAATGGAACCAA
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT
ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTATGTGTCTCT
GGGAATTGTGGGATTGGCAACTACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTGACATGG
AGAGAATTTCACTATATTCAGGTAAATAATATATAAAATAACCTAAGAGGTAAATCTTCTTTTGTGTTTATGAT
ATAGAATATGTTGACTTTACCCATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTGTTCCAATT
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTCCTAGACATAAATAAAGGCAT
TAAAATATTCTTTGTTTTTTTTTTTTTGTGTTGTTGTTTTGTTGTTGTTGTTTTGTTGTTGTTTTGAGATGAAGTCTCG
CTCTGTTGCCCATGCTGGAGTACAGTGGCAGCATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATT
TCTTGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTTAGTA
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC
AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAACTTGTTAGACAATTT
GCTACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTTATTATTCTTAAAAAAATATTCTTTTACC
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACCTAGCACTTTCAGAAACAAAACTCTCTCCTTGAAA
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT
ACTTACTCACTGAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGCTGACAAGATTCAAAGGACTAAA
TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT
CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCCCTAATTTGTAGGTTTCAG
CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTCTTTCACACATTGCTCTGCCTGTTACACATATGA
TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACCTGAGCCTATTCTACTATATGTACA

FIG. 4B

ATACCTAGCCATAATAGGTATACAATACACATTTGGTAAACTAATTTTCAACCAATGACATGTATTTTCAACT
AGTAACCTAGAAATGTTTCACTTAAAATCTGAGAACTGGTTACTACAAGTTACCTTGGAGATTCATATATGAAA
ACGCAAACCTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT
GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT
TGAGATTACATAGGTGAACAACATTTTTAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA
ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTTCATATTATTTCCATGTTATC
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAAATCAGAGTGAATCA
CATTAGTCGCCTTCACAACCTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT
TTAATTGAGAATCTAAAATGTACAAATCATTGTGTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT
GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAATAAATATCATAAG
GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG
TTCACCTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCCAAAAGAGCAGAAAGATG
TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG
ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTCTTTTGCGAGAGCAAGCTAGGA
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG
TATGGTATACACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGCTCCTGATATTTAAAGCATACTATT
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACCTGAG
ATATGTTCCAGTTGTAGAAATTACTGTTTACACACATTTTGTTCATATTGATATATTTTATCACCAACATTTCA
AGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:4)

FIG. 5

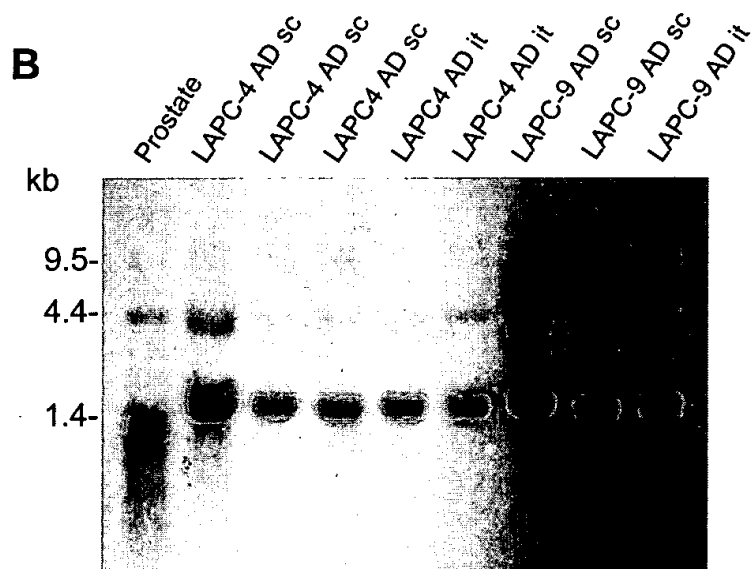
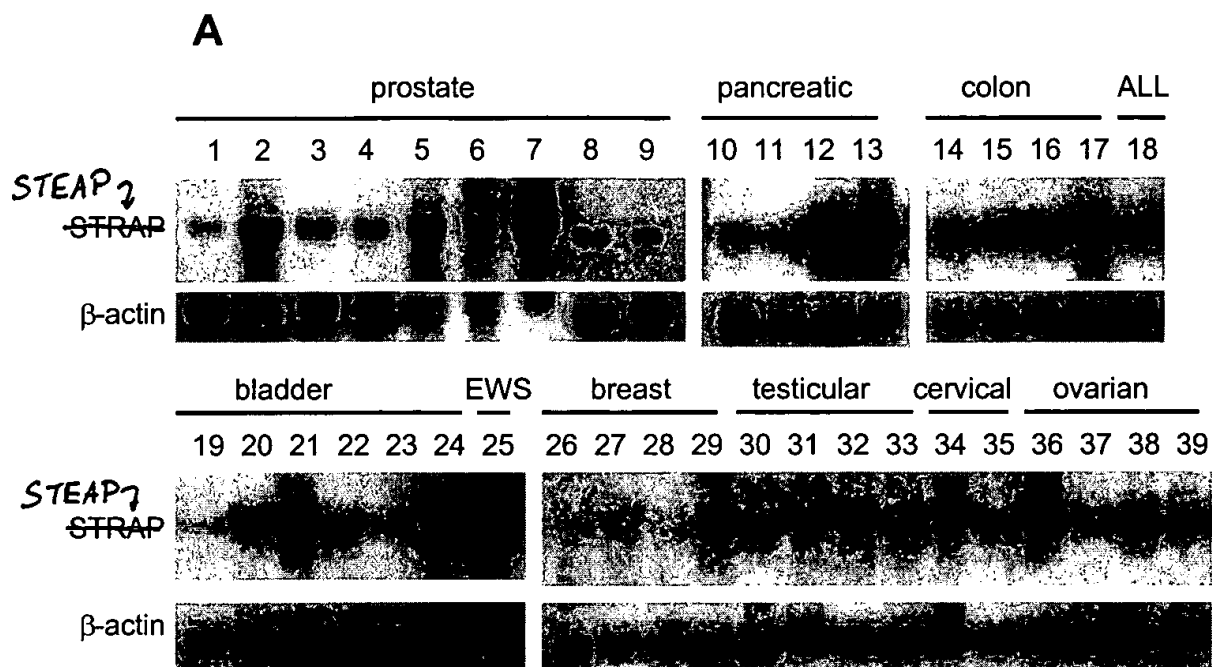


FIG. 6

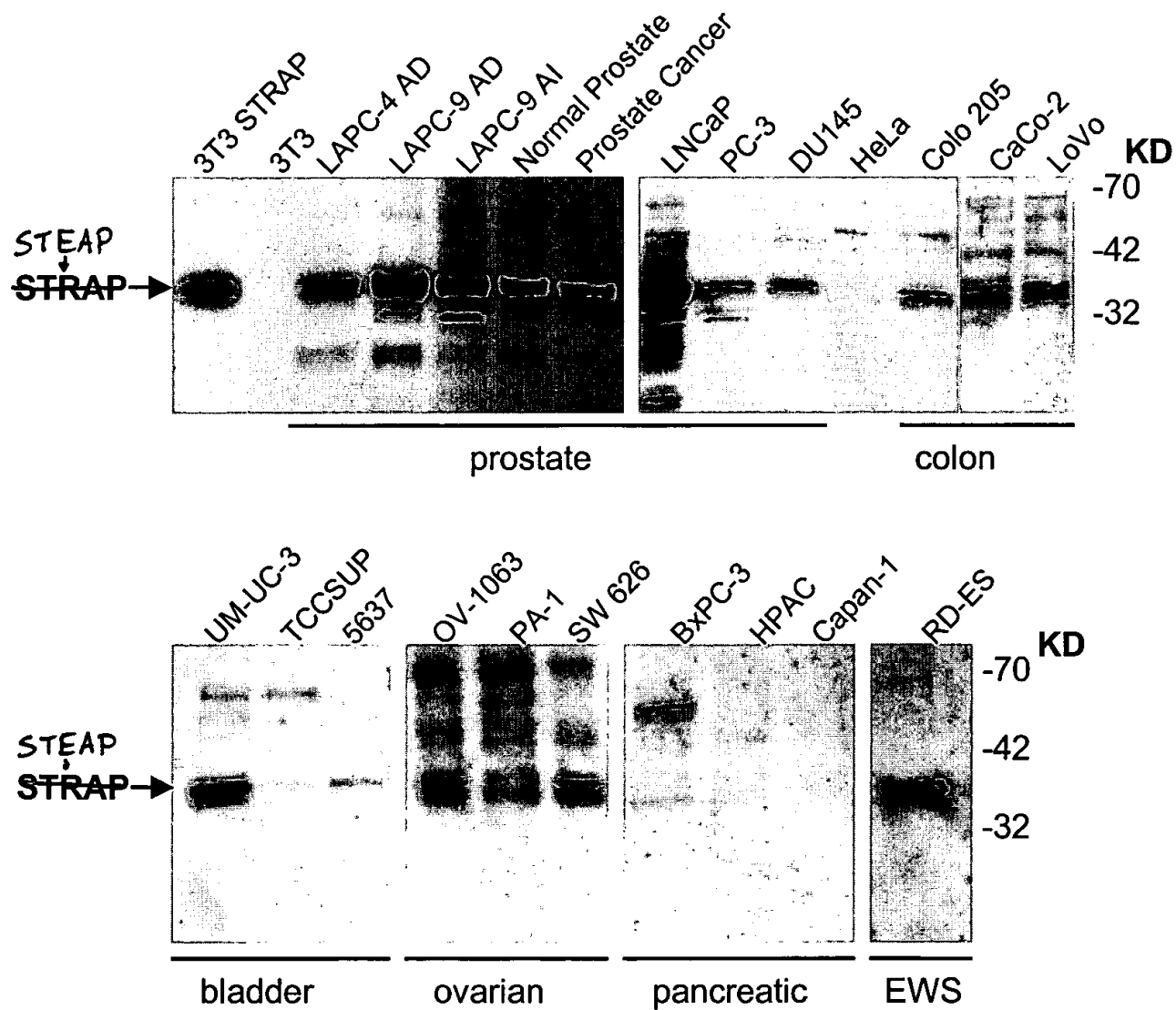
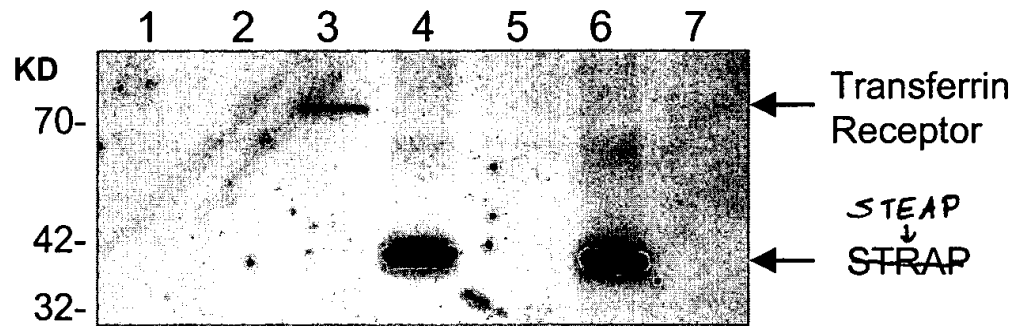


FIG. 7

A



B

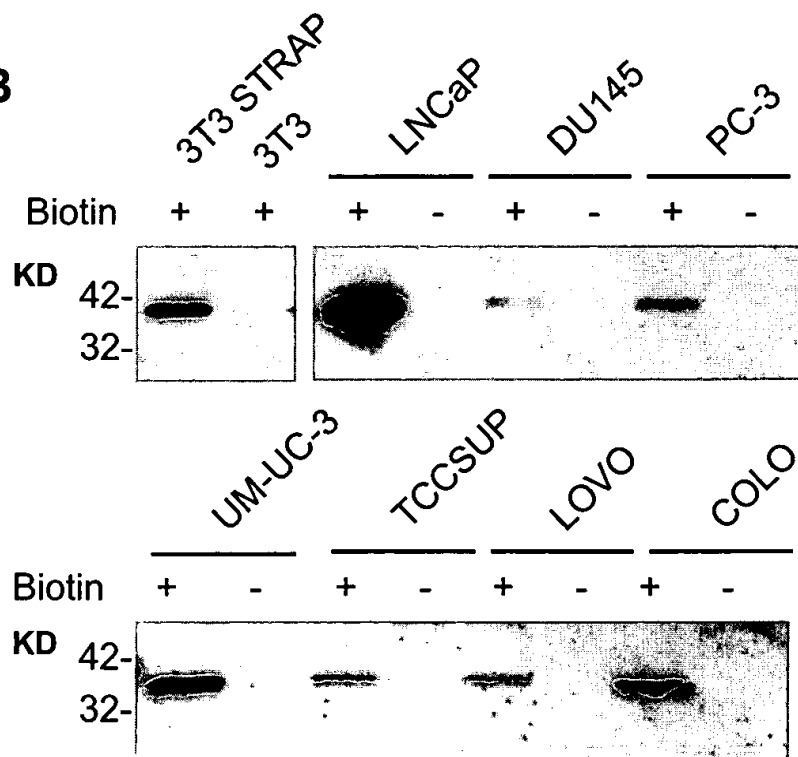


FIG. 9A

(SEQ ID NO: 5)																		
5'	10	19	28	37	46	55												
GGA	CGC	GTG	GGC	GGA	CGC	GTG	GGT	TCC	TCG	GGC	CCT	CGG	CGC	CAC	AAG	CTG	TCC	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	64	73	82	91	100	109												
GGG	CAC	GCA	GCC	CCT	AGC	GGC	GCG	TCG	CTG	CCA	AGC	CGG	CCT	CCG	CGC	GCC	TCC	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	118	127	136	145	154	163												
CTC	CTT	CCT	TCT	CCC	CTG	GCT	GTT	CGC	GAT	CCA	GCT	TGG	GTA	GGC	GGG	GAA	GCA	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	172	181	190	199	208	21												
GCT	GGA	GTG	CGA	CCG	CCA	CGG	CAG	CCA	CCC	TGC	AAC	CGC	CAG	TCG	GAG	GTG	CAG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	226	235	244	253	262	271												
TCC	GTA	GGC	CCT	GGC	CCC	CGG	GTG	GGC	CCT	TGG	GGA	GTC	GGC	GCC	GCT	CCC	GAG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	280	289	298	307	316	325												
GAG	CTG	CAA	GGC	TCG	CCC	CTG	CCC	GGC	GTG	GAG	GGC	GCG	GGG	GGC	GCG	GAG	GAT	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	334	343	352	361	370	379												
ATT	CTT	GGT	GAT	CTT	GGA	AGT	GTC	CGT	ATC	ATG	GAA	TCA	ATC	TCT	ATG	ATG	GGA	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
(SEQ ID NO: 6) →																		
				E	S	I	S	M	M	G								
	388	397	406	415	424	433												
AGC	CCT	AAG	AGC	CTT	AGT	GAA	ACT	TGT	TTA	CCT	AAT	GGC	ATA	AAT	GGT	ATC	AAA	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S	P	K	S	L	S	E	T	C	L	P	N	G	I	N	G	I	K	
	442	451	460	469	478	487												
GAT	GCA	AGG	AAG	GTC	ACT	GTA	GGT	GTG	ATT	GGA	AGT	GGA	GAT	TTT	GCC	AAA	TCC	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D	A	R	K	V	T	V	G	V	I	G	S	G	D	F	A	K	S	
	496	505	514	523	532	541												
TTG	ACC	ATT	CGA	CTT	ATT	AGA	TGC	GGC	TAT	CAT	GTG	GTC	ATA	GGA	AGT	AGA	AAT	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L	T	I	R	L	I	R	C	G	Y	H	V	V	I	G	S	R	N	
	550	559	568	577	586	595												
CCT	AAG	TTT	GCT	TCT	GAA	TTT	TTT	CCT	CAT	GTG	GTA	GAT	GTC	ACT	CAT	CAT	GAA	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
P	K	F	A	S	E	F	F	P	H	V	V	D	V	T	H	H	E	
	604	613	622	631	640	649												
GAT	GCT	CTC	ACA	AAA	ACA	AAT	ATA	ATA	TTT	GTT	GCT	ATA	CAC	AGA	GAA	CAT	TAT	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D	A	L	T	K	T	N	I	I	F	V	A	I	H	R	E	H	Y	
	658	667	676	685	694	703												
ACC	TCC	CTG	TGG	GAC	CTG	AGA	CAT	CTG	CTT	GTG	GGT	AAA	ATC	CTG	ATT	GAT	GTG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
T	S	L	W	D	L	R	H	L	L	V	G	K	I	L	I	D	V	
	712	721	730	739	748	757												
AGC	AAT	AAC	ATG	AGG	ATA	AAC	CAG	TAC	CCA	GAA	TCC	AAT	GCT	GAA	TAT	TTG	GCT	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S	N	N	M	R	I	N	Q	Y	P	E	S	N	A	E	Y	L	A	

766 775 784 793 802 811
TCA TTA TTC CCA GAT TCT TTG ATT GTC AAA GGA TTT AAT GTT GTC TCA GCT TGG
S L F P D S L I V K G F N V V S A W

820 829 838 847 856 865
GCA CTT CAG TTA GGA CCT AAG GAT GCC AGC CGG CAG GTT TAT ATA TGC AGC AAC
A L Q L G P K D A S R Q V Y I C S N

874 883 892 901 910 919
AAT ATT CAA GCG CGA CAA CAG GTT ATT GAA CTT GCC CGC CAG TTG AAT TTC ATT
N I Q A R Q Q V I E L A R Q L N F I

928 937 946 955 964 973
CCC ATT GAC TTG GGA TCC TTA TCA TCA GCC AGA GAG ATT GAA AAT TTA CCC CTA
P I D L G S L S S A R E I E N L P L

982 991 1000 1009 1018 1027
CGA CTC TTT ACT CTC TGG AGA GGG CCA GTG GTG GTA GCT ATA AGC TTG GCC ACA
R L F T L W R G P V V V A I S L A T

1036 1045 1054 1063 1072 1081
TTT TTT TTC CTT TAT TCC TTT GTC AGA GAT GTG ATT CAT CCA TAT GCT AGA AAC
F F F L Y S F V R D V I H P Y A R N

1090 1099 1108 1117 1126 1135
CAA CAG AGT GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT
Q Q S D F Y K I P I E I V N K T L P

1144 1153 1162 1171 1180 1189
ATA GTT GCC ATT ACT TTG CTC TCC CTA GTA TAC CTT GCA GGT CTT CTG GCA GCT
I V A I T L L S L V Y L A G L L A A

1198 1207 1216 1225 1234 1243
GCT TAT CAA CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA
A Y Q L Y Y G T K Y R R F P P W L E

1252 1261 1270 1279 1288 1297
ACC TGG TTA CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG
T W L Q C R K Q L G L L S F F F A M

1306 1315 1324 1333 1342 1351
GTC CAT GTT GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG
V H V A Y S L C L P M R R S E R Y L

1360 1369 1378 1387 1396 1405
TTT CTC AAC ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT
F L N M A Y Q Q V H A N I E N S W N

1414 1423 1432 1441 1450 1459
GAG GAA GAA GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT
E E E V W R I E M Y I S F G I M S L

FIG. 9B

1468 1477 1486 1495 1504 1513
GGC TTA CTT TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GAG AGC AAT GCT TTA

G L L S L L A V T S I P S V S N A L

1522 1531 1540 1549 1558 1567
AAC TGG AGA GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC

N W R E F S F I Q S T L G Y V A L L

1576 1585 1594 1603 1612 1621
ATA AGT ACT TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT TTT GAG GAA GAG

I S T F H V L I Y G W K R A F E E E

1630 1639 1648 1657 1666 1675
TAC TAC AGA TTT TAT ACA CCA CCA AAC TTT GTT CTT GCT CTT GTT TTG CCC TCA

Y Y R F Y T P P N F V L A L V L P S

1684 1693 1702 1711 1720 1729
ATT GTA ATT CTG GAT CTT TTG CAG CTT TGC AGA TAC CCA GAC TGA GCT GGA ACT

I V I L D L L Q L C R Y P D *

1738 1747 1756 1765 1774 1783
GGA ATT TGT CTT CCT ATT GAC TCT ACT TCT TTA AAA GCG GCT GCC CAT TAC ATT

1792 1801 1810 1819 1828 1837
CCT CAG CTG TCC TTG CAG TTA GGT GTA CAT GTG ACT GAG TGT TGG CCA GTG AGA

1846 1855 1864 1873 1882 1891
TGA AGT CTC CTC AAA GGA AGG CAG CAT GTG TCC TTT TTC ATC CCT TCA TCT TGC

1900 1909 1918 1927 1936 1945
TGC TGG GAT TGT GGA TAT AAC AGG AGC CCT GGC AGC TGT CTC CAG AGG ATC AAA

1954 1963 1972 1981 1990 1999
GCC ACA CCC AAA GAG TAA GGC AGA TTA GAG ACC AGA AAG ACC TTG ACT ACT TCC

2008 2017 2026 2035 2044 2053
CTA CTT CCA CTG CTT TTC CTG CAT TTA AGC CAT TGT AAA TCT GGG TGT GTT ACA

2062 2071 2080 2089 2098 2107
TGA AGT GAA AAT TAA TTC TTT CTG CCC TTC AGT TCT TTA TCC TGA TAC CAT TTA

2116 2125 2134 2143 2152 2161
ACA CTG TCT GAA TTA ACT AGA CTG CAA TAA TTC TTT CTT TTG AAA GCT TTT AAA

2170 2179 2188 2197 2206 2215
GGA TAA TGT GCA ATT CAC ATT AAA ATT GAT TTT CCA TTG TCA ATT AGT TAT ACT

2224 2233 2242 2251 2260 2269
CAT TTT CCT GCC TTG ATC TTT CAT TAG ATA TTT TGT ATC TGC TTG GAA TAT ATT

2278 2287 2296 2305 2314 2323
ATC TTC TTT TTA ACT GTG TAA TTG GTA ATT ACT AAA ACT CTG TAA TCT CCA AAA

2332 2341 2350 2359 2368 2377
TAT TGC TAT CAA ATT ACA CAC CAT GTT TTC TAT CAT TCT CAT AGA TCT GCC TTA

2386 2395 2404 2413 2422 2431
TAA ACA TTT AAA TAA AAA GTA CTA TTT AAT GAT TTA AAA AAA AAA AAA AAA AAA

2440 2449
AAA AAA AAA AAA AAA AAA AAA AA 3'

FIG. 9C

FIG. 10A-1

(SEQ ID NO: 7)

1 CGAAACTTCC CTCTACCCGC CCGGCCCGCG GCGCGCACCG TTGGCGCTGG ACGCTTCCTC
GCTTTGAAGG GAGATGGGCG GGCCGGGCGC CGCGCGTGCG AACCGCGACC TCGAAGGAG

(SEQ ID NO: 8)

61 CTTGGAAGCG CCTCTCCCTC AGTTATGGAG AAAACTTGTA TAGATGCACT TCCTCTTACT
GAACCTTCGC GGAGAGGGAG TCAATACCTC TTTTGAACAT ATCTACGTGA AGGAGAATGA

121 M N S S E K Q E T V C I F G T G D F G R
ATGAATTCTT CAGAAAAGCA AGAGACTGTA TGTATTTTTG GAACTGGTGA TTTTGAAGA
TACTTAAGAA GTCTTTTCGT TCTCTGACAT ACATAAAAAAC CTTGACCACT AAAACCTTCT

181 S L G L K M L Q C G Y S V V F G S R N P
TCACTGGGAT TGAAAATGCT CCAGTGTGGT TATTCTGTTG TTTTGGGAAG TCGAAACCCC
AGTGACCCTA ACTTTTACGA GGTCACACCA ATAAGACAAC AAAACCTTC AGCTTTGGGG

241 Q K T T L L P S G A E V L S Y S E A A K
CAGAAGACCA CCCTACTGCC CAGTGGTGCA GAACTCTTGA GCTATTCAGA AGCAGCCAAG
GTCTTCTGGT GGGATGACGG GTCACCACGT CTTCAGAACT CGATAAGTCT TCGTCGGTTC

301 K S G I I I I A I H R E H Y D F L T E L
AAGTCTGGCA TCATAATCAT AGCAATCCAC AGAGAGCATT ATGATTTTCT CACAGAATTA
- TTCAGACCGT AGTATTAGTA TCGTTAGGTG TCTCTCGTAA TACTAAAAGA GTGTCTTAAT

361 T E V L N G K I L V D I S N N L K I N Q
ACTGAGGTTT TCAATGGAAA AATATTGGTA GACATCAGCA ACAACCTCAA AATCAATCAA
TGACTCCAAG AGTTACCTTT TTATAACCAT CTGTAGTCGT TGTGGAGTT TTAGTTAGTT

421 Y P E S N A E Y L A H L V P G A H V V K
TATCCAGAAT CTAATGCAGA GTACCTTGCT CATTTGGTGC CAGGAGCCCA CGTGGTAAAA
ATAGGTCTTA GATTACGTCT CATGGAACGA GTAAACCACG GTCCTCGGGT GCACCATTTT

481 A F N T I S A W A L Q S G A L D A S R Q
GCATTTAACA CCATCTCAGC CTGGGCTCTC CAGTCAGGAG CACTGGATGC AAGTCGGCAG
CGTAAATTGT GGTAGAGTCG GACCCGAGAG GTCAGTCCTC GTGACCTACG TTCAGCCGTC

541 V F V C G N D S K A K Q R V M D I V R N
GTGTTTGTGT GTGGAAATGA CAGCAAAGCC AAGCAAAGAG TGATGGATAT TGTTCGTAAT
CACAAACACA CACCTTTACT GTCGTTTCGG TTCGTTTCTC ACTACCTATA ACAAGCATTA

601 L G L T P M D Q G S L M A A K E I E K Y
CTTGGACTTA CTCCAATGGA TCAAGGATCA CTCATGGCAG CCAAAGAAAT TGAAAAGTAC
GAACCTGAAT GAGGTTACCT AGTTCCTAGT GAGTACCGTC GGTTTCTTTA ACTTTTCATG

661 P L Q L F P M W R F P F Y L S A V L C V
CCCCTGCAGC TATTTCCAAT GTGGAGGTTT CCCTTCTATT TGTCTGCTGT GCTGTGTGTC
GGGGACGTCG ATAAAGGTTA CACCTCCAAG GGAAGATAA ACAGACGACA CGACACACAG

721 F L F F Y C V I R D V I Y P Y V Y E K K
TTCTTGTTTT TCTATTGTGT TATAAGAGAC GTAATCTACC CTTATGTTTA TGAAAAGAAA
AAGAACAAAA AGATAACACA ATATTCTCTG CATTAGATGG GAATACAAAT ACTTTTCTTT

D N T F R M A I S I P N R I F P I T A L
 781 GATAATACAT TTCGTATGGC TATTTCCATT CCAAATCGTA TCTTTCCAAT AACAGCACTT
 CTATTATGTA AAGCATACCG ATAAAGGTAA GGTTAGCAT AGAAAGGTTA TTGTCGTGAA

 T L L A L V Y L P G V I A A I L Q L Y R
 841 ACACTGCTTG CTTTGGTTTA CCTCCCTGGT GTTATTGCTG CCATTCTACA ACTGTACCGA
 TGTGACGAAC GAAACCAAAT GGAGGGACCA CAATAACGAC GGTAAGATGT TGACATGGCT

 G T K Y R R F P D W L D H W M L C R K Q
 901 GGCACAAAAT ACCGTCGATT CCCAGACTGG CTTGACCACT GGATGCTTTG CCGAAAGCAG
 CCGTGTTTTA TGGCAGCTAA GGGTCTGACC GAACTGGTGA CCTACGAAAC GGCTTTTCGT

 L G L V A L G F A F L H V L Y T L V I P
 961 CTTGGCTTGG TAGCTCTGGG ATTTGCCTTC CTTTCATGTCC TCTACACACT TGTGATTCCCT
 GAACCGAACC ATCGAGACCC TAAACGGAAG GAAGTACAGG AGATGTGTGA AACTAAGGA

 I R Y Y V R W R L G N L T V T Q A I L K
 1021 ATTCGATATT ATGTACGATG GAGATTGGGA AACTTAACCG TTACCCAGGC AATACTCAAG
 TAAGCTATAA TACATGCTAC CTCTAACCTT TTGAATTGGC AATGGGTCCG TTATGAGTTC

 K E N P F S T S S A W L S D S Y V A L G
 1081 AAGGAGAATC CATTAGCAC CTCCTCAGCC TGGCTCAGTG ATTCATATGT GGCTTTGGGA
 TTCCTCTTAG GTAAATCGTG GAGGAGTCGG ACCGAGTCAC TAAGTATACA CCGAAACCCT

 I L G F F L F V L L G I T S L P S V S N
 1141 ATACTTGGGT TTTTCTGTG TGTACTCTTG GGAATCACTT CTTTGCCATC TGTTAGCAAT
 TATGAACCCA AAAAAGACAA ACATGAGAAC CCTTAGTGAA GAAACGGTAG ACAATCGTTA

 A V N W R E F R F V Q S K L G Y L T L I
 1201 GCAGTCAACT GGAGAGAGTT CCGATTTGTC CAGTCCAAAC TGGGTTATTT GACCCTGATC
 CGTCAGTTGA CCTCTCTCAA GGCTAAACAG GTCAGGTTTG ACCCAATAAA CTGGGACTAG

 L C T A H T L V Y G G K R F L S P S N L
 1261 TTGTGTACAG CCCACACCCT GGTGTACGGT GGGAAGAGAT TCCTCAGCCC TTCAAATCTC
 AACACATGTC GGGTGTGGGA CCACATGCCA CCCTTCTCTA AGGAGTCGGG AAGTTTAGAG

 R W Y L P A A Y V L G L I I P C T V L V
 1321 AGATGGTATC TTCCTGCAGC CTACGTGTTA GGGCTTATCA TTCCTTGCAC TGTGCTGGTG
 TCTACCATAG AAGGACGTCG GATGCACAAT CCCGAATAGT AAGGAACGTG ACACGACCAC

 I K F V L I M P C V D N T L T R I R Q G
 1381 ATCAAGTTTG TCCTAATCAT GCCATGTGTA GACAACACCC TTACAAGGAT CCGCCAGGGC
 TAGTTCAAAC AGGATTAGTA CGGTACACAT CTGTTGTGGG AATGTTCCCTA GGCGGTCCCG

 W E R N S K H
 1441 TGGGAAAGGA ACTCAAAACA CTAGAAAAG CATTGAATGG AAAATCAATA TTTAAAACAA
 ACCCTTTCCT TGAGTTTGT GATCTTTTTC GTAACCTACC TTTTAGTTAT AAATTTTGT

 1501 AGTTCAATTT AGCTGGATTT CTGAACTATG GTTTTGAATG TTTAAAGAAG AATGATGGGT
 TCAAGTTAA TCGACCTAAA GACTTGATAC CAAAACCTAC AAATTTCTTC TTAACCTACA

 1561 ACAGTTAGGA AAGTTTTTTT CTTACACCGT GACTGAGGGA AACATTGCTT GTCTTTGAGA
 TGTCAATCCT TTCAAAAAA GAATGTGGCA CTGACTCCCT TTGTAACGAA CAGAAACTCT

 1621 AATTGACTGA CATACTGGAA GAGAACACCA TTTTATCTCA GGTTAGTGAA GAATCAGTGC
 TTAAGTACT GTATGACCTT CTCTTGTGGT AAAATAGAGT CCAATCACTT CTTAGTCACG

FIG. 10A-2

1681	AGGTCCTGA	C...TTATTTT	CCCAGAGGCC	ATGGAGCTGA	G...TGAGACT	AGCCTTGTGG
	TCCAGGGACT	GAGAATAAAA	GGGTCTCCGG	TACCTCGACT	CTAACTCTGA	TCGGAACACC
1741	TTTCACACTA	AAGAGTTTCC	TTGTTATGGG	CAACATGCAT	GACCTAATGT	CTTGCAAAAT
	AAAGTGTGAT	TTCTCAAAGG	AACAATACCC	GTTGTACGTA	CTGGATTACA	GAACGTTTTA
1801	CCAATAGAAG	TATTGCAGCT	TCCTTCTCTG	GCTCAAGGGC	TGAGTTAAGT	GAAAGGAAAA
	GGTTATCTTC	ATAACGTCGA	AGGAAGAGAC	CGAGTTCCCG	ACTCAATTCA	CTTTCCTTTT
1861	ACAGCACAAT	GGTGACCACT	GATAAAGGCT	TTATTAGGTA	TATCTGAGGA	AGTGGGTCAC
	TGTCGTGTTA	CCACTGGTGA	CTATTTCCGA	AATAATCCAT	ATAGACTCCT	TCACCCAGTG
1921	ATGAAATGTA	AAAAGGGAAT	GAGGTTTTTG	TTGTTTTTTG	GAAGTAAAGG	CAAACATAAA
	TACTTTACAT	TTTTCCCTTA	CTCCAAAAAC	AACAAAAAAC	CTTCATTGCC	GTTTGTATTT
1981	TATTACCATG	ATGAATTCTA	GTGAAATGAC	CCCTTGACTT	TGCTTTTCTT	AATACAGATA
	ATAATGGTAC	TACTTAAGAT	CACTTTACTG	GGGAAGTAA	ACGAAAAGAA	TTATGTCTAT
2041	TTTACTGAGA	GGAACATTTT	TTATAACACA	AGAAAAATTT	ACAATTGATT	AAAAGTATCC
	AAATGACTCT	CCTTGATAAA	AATATTGTGT	TCTTTTAA	TGTTAACTAA	TTTTCATAGG
2101	ATGTCTTGGA	TACATACGTA	TCTATAGAGC	TGGCATGTAA	TTCTTCCTCT	ATAAAGAATA
	TACAGAACCT	ATGTATGCAT	AGATATCTCG	ACCGTACATT	AAGAAGGAGA	TATTTCTTAT
2161	GGTATAGGAA	AGACTGAATA	AAAATGGAGG	GATATCCCCT	TGGATTTTAC	TTGCATTGTG
	CCATATCCTT	TCTGACTTAT	TTTTACCTCC	CTATAGGGGA	ACCTAAAGTG	AACGTAACAC
2221	CAATAAGCAA	AGAAGGGTTG	ATAAAAGTTC	TTGATCAAAA	AGTTCAAAGA	AACCAGAATT
	GTTATTCGTT	TCTTCCCAAC	TATTTTCAAG	AAGTAGTTTT	TCAAGTTTCT	TTGGTCTTAA
2281	TTAGACAGCA	AGCTAAATAA	ATATTGTAAA	ATTGCACTAT	ATTAGGTTAA	GTATTATTTA
	AATCTGTCGT	TCGATTATTT	TATAACATTT	TAACGTGATA	TAATCCAATT	CATAATAAAT
2341	GGTATTATAA	TATGCTTTGT	AAATTTTATA	TTCCAAATAT	TGCTCAATAT	TTTTCATCTA
	CCATAATATT	ATACGAAACA	TTTAAAATAT	AAGGTTTATA	ACGAGTTATA	AAAAGTAGAT
2401	TTAAATTAAT	TTCTAGTGTA	AATAAGTAGC	TTCTATATCT	GTCTTAGTCT	ATTATAATTG
	AATTTAATTA	AAGATCACAT	TTATTCATCG	AAGATATAGA	CAGAATCAGA	TAATATTAAC
2461	TAAGGAGTAA	AATTAAATGA	ATAGTCTGCA	GGTATAAATT	TGAACAATGC	ATAGATGATC
	ATTCCTCATT	TTAATTTACT	TATCAGACGT	CCATATTTAA	ACTTGTTACG	TATCTACTAG
2521	GAAAATTACG	GAAAATCATA	GGGCAGAGAG	GTGTGAAGAT	TCATCATTAT	GTGAAATTTG
	CTTTTAATGC	CTTTTAGTAT	CCCGTCTCTC	CACACTTCTA	AGTAGTAATA	CACTTTAAAC
2581	GATCTTTCTC	AAATCCTTGC	TGAAATTTAG	GATGGTTCTC	ACTGTTTTTC	TGTGCTGATA
	CTAGAAAAGAG	TTTAGGAACG	ACTTTAAATC	CTACCAAGAG	TGACAAAAAG	ACACGACTAT
2641	GTACCCTTTC	CAAGGTGACC	TTCAGGGGGA	TTAACCTTCC	TAGCTCAAGC	AATGAGCTAA
	CATGGGAAAG	GTTCCACTGG	AAGTCCCCCT	AATTGGAAGG	ATCGAGTTTC	TTACTCGATT
2701	AAGGAGCCTT	ATGCATGATC	TTCCACATA	TCAAAATAAC	TAAAAGGCAC	TGAGTTTGGC
	TTCTTCGGAA	TACGTACTAG	AAGGGTGTAT	AGTTTTATTG	ATTTTCCGTG	ACTCAAACCG
2761	ATTTTTCTGC	CTGCTCTGCT	AAGACCTTTT	TTTTTTTTTT	ACTTTTCATTA	TAACATATTA
	TAAAAAGACG	GACGAGACGA	TTCTGGAAAA	AAAAAAAAAA	TGAAAGTAAT	ATTGTATAAT

FIG. 10A-3

2821 TACATGACAT T. ACAAAAA TGATTAAAAT ATATTAAAAC A. ATCAACA ATCCAGGATA
 ATGTACTGTA ATATGTTTTT ACTAATTTTA TATAATTTTG TTGTAGTTGT TAGGTCCTAT
 2881 TTTTCTATA AAACTTTTTA AAAATAATTG TATCTATATA TTCAATTTTA CATCCTTTTT
 AAAAAGATAT TTTGAAAAAT TTTTATTAAC ATAGATATAT AAGTTAAAAT GTAGGAAAAA
 2941 CAAAGGCTTT GTTTTCTAA AGGCTTTGTT TTCCTTTTTA TTATTTTTTT CTTTTTTATT
 GTTCCGAAA CAAAAAGATT TCCGAAACAA AAGGAAAAAT AATAAAAAA GAAAAATAA
 3001 TTTTGGAGAC AGTCTTGCTC TGTCGCTCAG GCTGGAGTGC AGTGGCACGA TCTCAGCTCA
 AAAAATCTG TCAGAACGAG ACAGCGAGTC CGACCTCACG TCACCGTGCT AGAGTCGAGT
 3061 CTGCAACCTC CTCCTCCAG GTTCAAGTGA TTCTTGTTCA TCAGCCTCCC GAGTAGCTGG
 GACGTTGGAG GAGGAGGGTC CAAGTTCAC TAAACAAGT AGTCGGAGGG CTCATCGACC
 3121 GACTACAGGC ATGTGCCACT ATGCCAGCT AATTTTTGTA CTTTATAGTAG AGACAGGGTT
 CTGATGTCCG TACACGGTGA TACGGGTCGA TAAAAACAT GAAAATCATC TCTGTCCCAA
 3181 TCACCACATT GGTGAGGCTG GTCTTGAAAT GCTGGCGTCA AGTGATCTGC CTGCCTCCGC
 AGTGGTGTA CCAGTCCGAC CAGAACTTTA CGACCGCAGT TCACTAGACG GACGGAGGCG
 3241 CTTACGTAAT ATATTTTCTT AATGGCTGCA TAATATCACA TCAAATAGGC ATTTTCAAA
 GAATGCATTA TATAAAGAA TTACCGACGT ATTATAGTGT AGTTTATCCG TAAAAAGTTT
 3301 CCTCTTTCCT TATTAAACAT GTAGACTATA TCCATTTTTT ACTAAAATAA ATAACATTTT
 GGAGAAAGGA ATAATTTGTA CATCTGATAT AGGTAAAAA TGATTTTATT TATTGTAAAG
 3361 AGATAATATC TTTGCACTGA TAATGTTGCC AAGCCATTTT TAAAGTGACC TTATCAATTT
 TCTATTATAG AAACGTGACT ATTACAACGG TTCGGTAAAG ATTTCACTGG AATAGTTAAA
 3421 AATTACCATT GGATGAGGGT GTTGCTTTCA TCGCACCATT GTAGATTGTC TTTTTATTT
 TTAATGGTAA CCTACTCCCA CAACGAAAGT AGCGTGGTAA CATCTAACAG AAAAAATAA
 3481 CAATTTGCGT TTATTTATAA CTGGTTGCAA AGGTACACAG AACACACGCT CCTTCAACTT
 GTTAAACGCA AATAAATATT GACCAACGTT TCCATGTGTC TTGTGTGCGA GGAAGTTGAA
 3541 ATCTTTGATA AACCCAAGCA AGGATACAAA AAGTTGGACG ACATTGAGTA GAGTCATGGT
 TAGAACTAT TTGGGTTTCT TCCTATGTTT TTCAACCTGC TGTAACATCAT CTCAGTACCA
 3601 ATACGGTGCT GACCCTACAG TATCAGTGGA AAAGATAAGG AAAATGTCAC TACTCACCTA
 TATGCCACGA CTGGGATGTC ATAGTCACCT TTTCTATTCC TTTTACAGTG ATGAGTGGAT
 3661 TGTTATGCAA AACAGTTAGG TGTGCTGGGG CTGGATACTG CTCTTTTACT TGAGCATTGG
 ACAATACGTT TTGTCAATCC ACACGACCCC GACCTATGAC GAGAAAATGA ACTCGTAACC
 3721 TTGATTAAAG TTTAGGTACC ATCCAGGCTG GTCTAGAGAA GTCTTTGGAG TTAACCATGC
 AACTAATTTT AAATCCATGG TAGGTCCGAC CAGATCTCTT CAGAAACCTC AATTGGTACG
 3781 TCTTTTTGTT AAAGAAGAGA GTAATGTGTT TATCCTGGCT CATAGTCCGT CACCGAAAAA
 AGAAAAACAA TTTCTTCTCT CATTACACAA ATAGGACCGA GTATCAGGCA GTGGCTTTTA
 3841 AGAAAATGCC ATCCATAGGT AAAATGCTGA CCTATAGAAA AAAATGAACT CTACTTTTAT
 TCTTTTACGG TAGGTATCCA TTTTACGACT GGATATCTTT TTTTACTTGA GATGAAAATA
 3901 AGCCTAGTAA AAATGCTCTA CCTGAGTAGT TAAAGCAAT TCATGAAGCC TGAAGCTAAA
 TCGGATCATT TTTACGAGAT GGACTCATCA ATTTTCGTTA AGTACTTCGG ACTTCGATTT

FIG. 10A-4

3961 GAGCACTCTG A. JTTTTGG CATAATAGCT GCATTTCAG AC TGACCTT TGGCCCCAAC
 CTCGTGAGAC TACCAAAACC GTATTATCGA CGTAAAGGTC TGGACTGGAA ACCGGGGTTG
 4021 CACAAGTGCT CCAAGCCCCA CCAGCTGACC AAAGAAAGCC CAAGTTCTCC TTCTGTCCTT
 GTGTTACGA GGTCGGGGT GGTCGACTGG TTTCTTTCGG GTTCAAGAGG AAGACAGGAA
 4081 CCCACAACCT CCCTGCTCCC AAAACTATGA AATTAATTTG ACCATATTAA CACAGCTGAC
 GGGTGTTGGA GGGACGAGGG TTTTGATACT TTAATTAAAC TGGTATAATT GTGTCGACTG
 4141 TCCTCCAGTT TACTTAAGGT AGAAAGAATG AGTTTACAAC AGATGAAAAT AAGTGCTTTG
 AGGAGGTCAA ATGAATTCCA TCTTTCTTAC TCAAATGTTG TCTACTTTTA TTCACGAAAC
 4201 GGCGAAGTGT ATTCCTTTTA ACAGATCCAA ACTATTTTAC ATTTAAAAAA AAAGTTAAAC
 CCGCTTGACA TAAGGAAAAT TGTCTAGGTT TGATAAAATG TAAATTTTTT TTTCAATTTG
 4261 TAAACTTCTT TACTGCTGAT ATGTTTCCTG TATTCTAGAA AAATTTTTTAC ACTTTCACAT
 ATTTGAAGAA ATGACGACTA TACAAAGGAC ATAAGATCTT TTTAAAAATG TGAAAGTGTA
 4321 TATTTTTGTA CACTTTCCCC ATGTTAAGGG ATGATGGCTT TTATAAATGT GTATTCATTA
 ATAAAAACAT GTGAAAGGGG TACAATTCCC TACTACCGAA AATATTTACA CATAAGTAAT
 4381 AATGTTACTT TAAAAATAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
 TTACAATGAA ATTTTATTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

FIG. 10A-5

FIG. 10B

STEAP-2, AA508880 (NCI_CGAP Pr6)

ggtcgacttttctttattcctttgtcagagatctgattcatccatattgctagaaaccaacagagtgaacttttaca
aaattcctatagagattgtgaataaaaaccttacctatagttgccattactttgtctccttagtataccttgcagg
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttggttggaacctgggta
cagtgtagaaaacagcttggtactaagttgtttcttcgctatggtccatggtgcctacagcctctgcttaccga
tgagaagggtcagagagat (SEQ ID NO: 9)

STEAP-2, 98P4B6 SSH fragment

TTTGACGCTTTGCAGATACCCAGACTGAGCTGGAAGTGAATTTGTCTTCCTATTGACTCTACTTCTTTAAAGCG
GCTGCCATTACATTCTCAGCTGTCTTGACGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGTCCTTTT (SEQ ID NO: 10)

STEAP-3, AI139607 (testis EST)

aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaataacttgggtttt
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcaactggagagagttccgatttgt
ccagtcctaaactgggttatttgacctgatcttgtgtacagccacacctgggtgtacggtgggaagagattcctc
agcccttcaaatctcagatggtatcttctcgcagcctacgtgttagggcttatcattccttgcactgtgctggtga
tcaagtttgtcctaatacatgccatgtgtagacaacaccttacaaggatccgccagggtgggaagggaactcaaa
acactagaaaaagcattgaatggaaaatcaatattttaaacaagttcaatttagctggaaaaaaa
(SEQ ID NO: 11)

STEAP 4, R80991 (placental EST)

ggccgcggcanccgctacgacctggtcaacctggcagtcgaagcaggtcttggccanacaagagccacctctgggtg
aaggaggaggtctggcggtatggagatctacctctccctgggagtgctggccctcggcacgttgtccctgctggccg
tgacctcactgccgtccattgcaaactcgtcaactggaggaggttcagcttcgttcagtcctcactgggctttgt
ggcctcgtgctgagcacactncacacgctcacctacggctggaccgcgcttcgaggagagccgctacaagttc
tacctnccctcccaccttcacgntcacgctgctggtgacctgcgttcgttcacctcctgggccaagccctgttntac
tgccctgcattcagccgnaga (SEQ ID NO: 12)

FIG. 11A-1

[illegible]

FIG. 11A-2

	361	375	376	390	391	405	406	420	421	435	436	450
2 STEAP2	IEMXISFGIMSLGHI	SLLAVTSIPSVSNAL	NWREFFSFIQSTLGVV	ALNISTFHVLTYGMR	RAFESEVYREYTPEN	EVLAVVLE	-SIVL	LD				445
3 STEAP3	SDSKVAGILGFFIF	VHGIPTSLFESVBNV	NWREFFPVQSKLGYL	THILCTAHIVYGGK	RFLSPENLRWYLPAA	YVIGHIIPCTV	LVIR					434
4 STEAP1	MEIVVSLGVVGHAI	ALLAVTSIPSVSDSI	TWREHYIQSKLGIN	SLHGIHIALIFAWN	KWIDIKQFVWYTPPT	EMIAVFLI	IVVITFEK					305
5 STEAP4	MEIVLSLGVVAGTI	SLLAVTSIPSVIANSL	NWREFFPVQSSIGTN	AXVLSLHTITGWT	RAFESEERKATLPPPT	STXTLVLVE	-CRSSW					120

	451	465	466	480	481
2 STEAP2	LLQICRYPD	---	---	---	---
3 STEAP3	FVIMPGVDNLTTR	ROGWERNSEH	---	---	454
4 STEAP1	SLIFLPCLRKILKI	RHGWEDVTINKTEI	CSQL	---	459
5 STEAP4	AKATFXLPCIQPX	---	---	---	339
					133

FIG. 11B

STRAP-1	67	LFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPVMSITLL
STRAP-2	208	LFTLWRGPFVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLL
		** * * * * ** * * * * *
STRAP-1	127	ALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFVAVLHAIYSLSPMRR
STRAP-2	268	SLVYLAGLLAAAYQLYYGTKYRRFPWLETWLQCRKQLGLLSFFFAMVHVAYSCLPMRR
		**** * ** ** * * * * * * * * * * * * * * *
STRAP-1	187	SYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSLT
STRAP-2	328	SERYFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALN
		* ** * * * * * * * * * * * * * * * * *
STRAP-1	247	WREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVELPIVLI
STRAP-2	388	WREFSFIQSTLGYVALLISTFHVLIYGWKRAFEERYRFTPPNFVLALVLPISIVIL
		**** * * * * * * * * * * * * * * *

FIG. 11C

STEAP1 66 ELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPVMSITL

STEAP3 195 QLFPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTL
 *** * * * * * * * * *

STEAP1 126 LALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFVAVLHAIYSLSYPMR

STEAP3 255 LALVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIR
 ***** ** **** ** **** ** **** ** ** ** **

STEAP1 186 RSYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSL

STEAP3 315 YYVRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFLVLLGITSLSVSNVAV
 * * * * * * * * * * * * * *

STEAP1 246 TWREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLIKF

STEAP3 375 NWREFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAVVLGLIIPCTVLVIK
 ***** * * * * * * * * *

STEAP1 306 SILFLPCLRKKILKIRHWEDVTK

STEAP3 435 FVLIMPCVDNTLTRIRQGWERNK
 * * * * * *

FIG. 11D

STEAP2 29 RKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHEDALTKTNI

STEAP3 18 KQETVCIFGTGDFGRSLGLKMLQCGYSVVFGSRNPQ-KTTLPSGAEVLSYSEAAKSGI
 ** * *** ** **** * * *

STEAP2 89 IFVAIHREHYTSLWDLRHLLVGKILIDVSNMNRINQYPESNAEYLASLFPDSLIVKGFNV

STEAP3 77 IIIAIHREHYDFLTEVLNGKILVDISNNLKINQYPESNAEYLAHLVPGAHVVKAFNT
 * ***** * * * ***** * * ** **

STEAP2 149 VSAWALQLGPKDASRQVYICSNNIARQQVIELARQLNFIPIIDLGSLSAREIENLPLRL

STEAP3 137 ISAWALQSGALDASRQVFVCGNSKAKQVRMDIVRNGLTPMDQGSLSMAAKEIEKYPLQL
 ***** * ***** * * * * * * * * * * * * *

STEAP2 209 FTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPVAVITLLS

STEAP3 197 FPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFFITALTLLA
 * * * * * * * * * * * * * * * * *

STEAP2 269 LVYLAGLLAAAYQLYYGTKYRRFPWLETWLQCRKQLGLLSFFFAMVHVAYSCLCLPMRRS

STEAP3 257 LVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIRYY
 ***** * * * * * * * * * * * * * * * * *

STEAP2 329 ERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNW

STEAP3 317 VRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFVLLGITSLSVSNVAVNW
 * * * * * * * * * * * * * * * * *

STEAP2 389 REFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYRFTPPNFVLALVLPISIVIL

STEAP3 377 REFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAAYVLGLIIPCTVLV
 *** * * * * * * * * * * * * * * * *